

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 10:12:19 ; Search time 260.97 Seconds  
(without alignments)  
361.981 Million cell updates/sec

Title: US-10-717-984-1

Perfect score: 1149

Sequence: 1 MGKGDPKPRKMSYAFV.....DEEEDEDEDEDDDDDE 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	215	6 ABU07499	Abu07499 Protein d
2	1149	100.0	215	6 AAE35859	Aae35859 Human HMG
3	1149	100.0	215	7 ADD40789	Add40789 Human HMG
4	1149	100.0	215	7 ADD40788	Add40788 Human HMG
5	1149	100.0	215	7 ABM85677	Abm85677 Human pro
6	1149	100.0	215	8 ADO60491	Ado60491 Human hig
7	1149	100.0	215	8 ADO25918	Ado25918 Human hig
8	1149	100.0	215	8 ADO71477	Ado71477 Human hig
9	1149	100.0	215	8 ADR45922	Adr45922 Human hig
10	1149	100.0	215	8 ABM81508	Abm81508 Tumour-as
11	1149	100.0	215	9 ADW81011	Adw81011 Amphoteri
12	1149	100.0	215	9 ADX69343	Adx69343 Human amp
13	1149	100.0	215	9 ADY14248	Ady14248 PRO poly
14	1149	100.0	215	9 ADY85326	Ady85326 Human hig
15	1149	100.0	215	9 ADY85085	Ady85085 Human HMG
16	1149	100.0	215	9 ADZ80804	Adz80804 Amino aci
17	1144	99.6	214	7 ADD47645	Add47645 Human pro
18	1144	99.6	214	7 ADE60447	Ade60447 Human Pro
19	1144	99.6	214	7 ADE57980	Ade57980 Human Pro
20	1144	99.6	214	7 ADE57984	Ade57984 Human Pro
21	1144	99.6	214	7 ADE60732	Ade60732 Human Pro
22	1144	99.6	214	7 ADE60728	Ade60728 Human Pro
23	1144	99.6	214	8 ADS17580	Adsl7580 Amino aci
24	1144	99.6	221	9 ADY85051	Ady85051 Human HMG

25	1142	99.4	215	5 ABB57220	Abb57220 Mouse isc
26	1142	99.4	215	6 AAE35860	Aae35860 Mouse and
27	1142	99.4	215	7 ADD47643	Add47643 Rat Prote
28	1142	99.4	215	8 ADO25919	Ado25919 Mouse/rat
29	1142	99.4	215	8 ADO71478	Ado71478 Mouse/kat
30	1142	99.4	215	8 ADR87104	Adr87104 High Mobi
31	1142	99.4	215	9 ADY85327	Ady85327 Mouse and
32	1142	99.4	220	7 ABM85676	Abm85676 Mouse pro
33	1142	99.4	252	9 ADY85016	Ady85016 Human HMG
34	1140	99.2	215	9 ADY85029	Ady85029 Rat and m
35	1140	99.2	215	9 ADY85088	Ady85088 Human HMG
36	1140	99.2	229	5 ABP64829	Abp64829 Human pro
37	1137	99.0	214	7 ADE60730	Ade60730 Rat Prote
38	1137	99.0	214	7 ADE57978	Ade57978 Rat Prote
39	1137	99.0	214	7 ADE57982	Ade57982 Rat Prote
40	1137	99.0	214	7 ADE60726	Ade60726 Rat Prote
41	1137	99.0	214	7 ADE60445	Ade60445 Rat Prote
42	1135	98.8	215	8 ADO80179	Ado80179 High mobi
43	1129	98.3	215	9 AEA90125	Aea90125 Human hig
44	1122.5	97.7	216	6 AAE35866	Aae35866 Human HMG
45	1122.5	97.7	216	8 ADO25935	Ado25935 Wild type

#### ALIGNMENTS

##### RESULT 1

ABU07499  
ID ABU07499 standard; protein; 215 AA.  
AC ABU07499;  
XX  
XX  
DT DT  
XX 28-JAN-2003 (first entry)  
XX  
DE Protein differentially regulated in prostate cancer #102.  
XX  
KW Prostate cancer; gene expression; differential regulation;  
KW molecular marker; drug target; cancer detection; cancer diagnosis;  
KW cancer staging; cancer grading; cancer assessing; cancer monitoring.  
XX  
OS Homo sapiens.  
XX  
PN W0200281638-A2.  
XX  
PD 17-OCT-2002.  
XX  
PF 08-APR-2002; 2002WO-US010824.  
XX  
PR 06-APR-2001; 2001US-0281731P.  
PR 06-APR-2001; 2001US-0281732P.  
(ORIG-) ORIGENE TECHNOLOGIES INC.  
PI Sun Z, Jay G;  
XX  
DR WPI; 2003-058520/05.  
DR N-PSDB; ABX10404.  
XX  
PT Novel genes which are differentially regulated in prostate cancer, useful  
PT for diagnosing prostate cancer in prostate tissue sample and assessing  
PT therapeutic or preventive intervention in prostate cancer patients.  
XX  
PS  
XX  
XX  
CC Claim 1; Page 413-414; 416pp; English.  
CC  
CC The invention describes genes (I) which are differentially regulated in  
CC prostate cancer. (I) is useful for diagnosing a prostate cancer in a  
CC sample comprising prostate tissue, which involves determining the number  
CC of target genes which are differentially-regulated in the sample, where  
CC the number is indicative of the probability that the sample comprises  
CC prostate cancer. (I) is useful for assessing a therapeutic or preventive  
CC intervention in a subject having a prostate cancer, which involves  
CC determining the expression levels in a sample comprising prostate tissue  
CC of target genes which are differentially-regulated in prostate cancer.

CC Preferably, the expression levels of at least 10 genes are determined.  
CC (I) is also useful for identifying agents that modulate a biological  
CC activity of a polypeptide differentially-regulated in prostate cancer  
CC cells, which involves contacting a polypeptide differentially-regulated  
CC in prostate cancer cells with a test agent under conditions effective for  
CC the test agent to modulate a biological activity of the polypeptide, and  
CC determining whether the test agent modulates the biological activity. (I)  
CC is useful as molecular markers, as drug targets, and for detecting,  
CC diagnosing, staging, grading, assessing, monitoring, prognosticating,  
CC preventing or treating, determining predisposition to diseases and  
CC conditions especially relating to prostate cancer. (I) and its expression  
CC products are used in the diagnostic test to assay for presence of cancer  
CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in  
CC blood etc. (I) is useful for assessing cancer e.g., to determine the type  
CC of cancer, its stage of development, the nature of genetic defect, etc.  
CC The polypeptide encoded by (I) can be used as target for therapy or drug  
CC discovery. (I) can also be used for expressing the polypeptide and thus  
CC for searching specific binding partners of the polypeptide. (I) is useful  
CC in therapeutic applications to treat prostate cancer. The identification  
CC of specific genes, and groups of genes, expressed in pathways  
CC physiologically relevant to prostate cancer permits the definition of  
CC functional and disease pathways and the delineation of targets in these  
CC pathways which are useful in diagnostic, therapeutic, and clinical  
CC applications. This is the amino acid sequence of a protein differentially  
CC regulated in prostate cancer  
XX  
XX

XX Sequence 215 AA;  
Query Match 100.0%; Score 1149; DB 6; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.7e-93;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKGDPPKPRGKMSYAFFVQTCREHKKKHPPDASVNFSEFSKCSRWKMTSAKEGKGF 60  
DB 1 MGKGDPPKPRGKMSYAFFVQTCREHKKKHPPDASVNFSEFSKCSRWKMTSAKEGKGF 60  
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLCSEYRPKIKGEHPGL 120  
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLCSEYRPKIKGEHPGL 120  
QY 121 SIGDVAKKLGEMWNTAADKQPYEKKAAKLKEKYEKDIAAYRAKGPDAKKGVVKAKEK 180  
DB 121 SIGDVAKKLGEMWNTAADKQPYEKKAAKLKEKYEKDIAAYRAKGPDAKKGVVKAKEK 180  
QY 181 SKKKKEEEDDE 215  
DB 181 SKKKKEEEDDE 215

RESULT 2  
AAE35859 standard; protein; 215 AA.  
XX AAE35859;  
XX  
DT 17-JUN-2003 (first entry)  
XX  
DE Human HMGI protein.  
XX  
KW Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma;  
KW inflammatory cytokine; endotoxin shock; rheumatoid arthritis; hepatitis;  
KW appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis;  
KW allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis;  
KW emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis;  
KW Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes;  
KW Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease;  
KW anebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis;  
KW gene therapy; human immunodeficiency virus; HMGB1 protein.  
XX  
OS Homo sapiens.  
XX  
FH Binding-site 9. .85  
FT Key Location/Qualifiers

FT Binding-site /note= "DNA binding motif (HMG1 A box)"  
FT 89. .162  
XX /note= "DNA binding motif (HMG1 B box)"  
PN W0200292004-A2.  
XX  
XX 21-NOV-2002.  
XX  
XX 15-MAY-2002; 2002WO-US015329.  
XX  
XX 15-MAY-2001; 2001US-0291034P.  
XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (UVP1-) UNIV PITTSBURGH.  
XX  
PI Tracey KJ, Yang H, Warren HS, Fink MP;  
XX  
XX WPI; 2003-120594/11.  
XX  
XX New isolated polypeptide having a vertebrate HMG A box, useful for  
PT inhibiting a condition associated with an activated inflammatory cytokine  
PT cascade, e.g. endotoxin shock, myocardial infarction, asthma, HIV  
PT infection, malaria and diabetes.  
XX  
XX Disclosure; Fig 12A; 82pp; English.  
XX  
XX The invention relates to high mobility group (HMG) protein comprising DNA  
CC binding motifs termed HMG A box and HMG B box. HMG A box or a non-  
CC naturally occurring HMG A box inhibits the release of a pro-inflammatory  
CC cytokine from a vertebrate cell. The methods and compositions of the  
CC invention are useful for inhibiting a condition characterised by  
CC activation of an inflammatory cytokine cascade such as endotoxin shock,  
CC rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's  
CC disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,  
CC sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,  
CC filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,  
CC myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout,  
CC cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host  
CC disease, diabetes and Hodgkin's disease. The invention is useful in gene  
CC therapy. The present sequence is human HMGI (also termed as HMGB1)  
CC protein  
XX  
XX Sequence 215 AA;  
Query Match 100.0%; Score 1149; DB 6; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.7e-93;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKGDPPKPRGKMSYAFFVQTCREHKKKHPPDASVNFSEFSKCSRWKMTSAKEGKGF 60  
DB 1 MGKGDPPKPRGKMSYAFFVQTCREHKKKHPPDASVNFSEFSKCSRWKMTSAKEGKGF 60  
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLCSEYRPKIKGEHPGL 120  
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLCSEYRPKIKGEHPGL 120  
QY 121 SIGDVAKKLGEMWNTAADKQPYEKKAAKLKEKYEKDIAAYRAKGPDAKKGVVKAKEK 180  
DB 121 SIGDVAKKLGEMWNTAADKQPYEKKAAKLKEKYEKDIAAYRAKGPDAKKGVVKAKEK 180  
QY 181 SKKKKEEEDDE 215  
DB 181 SKKKKEEEDDE 215  
RESULT 3  
ADD40789  
ID ADD40789 standard; protein; 215 AA.  
XX  
AC ADD40789;  
XX  
DT 15-JAN-2004 (first entry)









OS	Homo sapiens.
XX	
XX	WO2004030615-A2.
PN	
XX	
XX	15-APR-2004.
PD	
XX	
XX	29-SEP-2003; 2003WO-US028547.
XX	
XX	02-OCT-2002; 2002US-0414971P.
PR	
XX	
XX	(GETH ) GENENTECH INC.
PA	
XX	
PI	Wu TD, Zhang Z, Zhou Y;
XX	
XX	WPI; 2004-347921/32.
DR	
DR	N-PSDB; ACN39623.
XX	
XX	New tumor-associated antigenic target polypeptides and nucleic acids,
PT	useful in preparing a medicament for treating or detecting a
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT	

```

PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 3888; 7273pp; English.
XX

The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1149; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTMSSAKEGKGF 60
Db 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTMSSAKEGKGF 60

Qy 61 EDMAKADKARYEREMKTYIIPKGTGTTKKFKDPNAPKPPPSAFFLFCSEYRPKIGEHPL 120
Db 61 EDMAKADKARYEREMKTYIIPKGTGTTKKFKDPNAPKPPPSAFFLFCSEYRPKIGEHPL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKDIAAYRAKGPDAAKGKGVVKA 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKDIAAYRAKGPDAAKGKGVVKA 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 11
ADW81011
XX ADW81011 standard; protein; 215 AA.
XX
AC ADW81011;
XX
DT 21-APR-2005 (first entry)
XX
DE Amphoterin protein sequence.
XX
KW Vascular endothelial growth factor; VEGF;
KW vascular endothelial growth factor receptor; VEGFR; dermatological;
KW edema; gene therapy; vulvar; injury; burn; skin cancer; cytostatic;
KW wound healing; hematoma; pain; necrosis; ischemia; vasotropic;
KW angiogenesis stimulation; vascularization; tissue regeneration;
KW amphoterin.
XX
OS Homo sapiens.
XX
PN WO2005011722-A2.
XX
PD 10-FEB-2005.
XX
PF 14-JUN-2004; 2004WO-US019197.
XX

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PR 12-JUN-2003; 2003US-0478114P.
PR 12-JUN-2003; 2003US-0478390P.
XX
FA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Saarikisto A, Karkkainen M, Tammela T, Asko-Seljavaara S;
PI Yla-Herttuala S, He Y;
XX
DR WPI; 2005-142834/15.
XX
PT Improving healing of skin graft or skin flap to underlying tissue useful
PT in mastopexy, cosmetic surgery, abdominoplasty, involves using
PT composition of vascular endothelial growth factor-C or D polynucleotides
PT and/or polypeptides.
XX
XX Example 11; SEQ ID NO 22; 119pp; English.
XX
XX The present invention relates to new vascular endothelial growth factor
XX (VEGF) proteins useful for skin healing of a skin graft onto underlying
XX tissue. The method involves contacting a skin graft/flap or underlying
XX tissue with an agent chosen from vascular endothelial growth factor C
XX (VEGF-C) polynucleotides, VEGF-C polypeptides, VEGF-D polynucleotides,
XX and VEGF-D polypeptides, in amount effective to reduce edema or increase
XX perfusion at skin graft or flap. The composition comprises a gene therapy
XX vector that encodes VEGF-C polynucleotide. The VEGF-C polypeptide
XX comprises the formula X-B-Z or Z-B-X, where X binds VEGF receptor-3
XX (VEGFR-3) and comprises a VEGFR-3 ligand amino acid sequence chosen from
XX a prepro-VEGF-C sequence, and fragments that binds VEGFR-3, where Z
XX comprises a heparin-binding amino acid sequence, and B comprises a
XX covalent attachment linking X to Z. The VEGF-C polynucleotides, VEGF-C
XX polypeptides, VEGF-D polynucleotides, and VEGF-D polypeptides comprise a
XX VEGF homology domain (VHD) and a heparin-binding domain. Vulnerary. Gene
XX therapy. The method is useful in treating skin injury such as burns or
XX skin cancer, skin grafts, cosmetic surgery, a liposuction procedure, or
XX in reconstructive surgery. The reconstructive surgery is breast
XX reconstruction following mastectomy or injury. The subject is diabetic.
XX The method is useful for improving post-surgical wound healing after
XX reconstructive and cosmetic surgery and improves complications resulting
XX from surgery which includes excessive bleeding, such as hematomas,
XX bruising and wound-healing difficulties, pain, edema, necrosis and
XX ischemia. The present sequence is amphoterin protein, which contains a
XX heparin binding domain related to the invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1149; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTMSSAKEGKGF 60
Db 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTMSSAKEGKGF 60

Qy 61 EDMAKADKARYEREMKTYIIPKGTGTTKKFKDPNAPKPPPSAFFLFCSEYRPKIGEHPL 120
Db 61 EDMAKADKARYEREMKTYIIPKGTGTTKKFKDPNAPKPPPSAFFLFCSEYRPKIGEHPL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKDIAAYRAKGPDAAKGKGVVKA 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKDIAAYRAKGPDAAKGKGVVKA 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 12
ADX69343
XX ID ADX69343 standard; protein; 215 AA.
XX
AC ADX69343;
XX
XX

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DT 05-MAY-2005 (first entry)  
XX Human amphoterin.  
XX amphoterin; Heparin binding protein; Neuroprotective; Nootropic;  
XX Antiparkinsonian; Anticonvulsant; VEGF-3 receptor;  
KW Angiogenesis stimulator; Gene Therapy;  
KW vascular endothelial growth factor receptor 3; VEGFR-3;  
KW angiogenesis disorder; neurodegenerative disorder; Alzheimers disease;  
KW Parkinsons disease; motor neurone disease; dementia; paralysis; VEGF-C;  
KW neurological disease; Huntingtons chorea;  
KW vascular endothelial growth factor receptor 3; neurological disease.  
XX  
OS Homo sapiens.  
XX  
XX W02005016963-A2.  
XX  
XX 24-FEB-2005.  
XX  
XX 14-JUN-2004; 2004WO-US019122.  
XX  
PR 12-JUN-2003; 2003US-0478114P.  
PR 12-JUN-2003; 2003US-0478390P.  
PR 23-SEP-2003; 2003US-00669176.  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
PA  
XX Alitalo K, He Y, Tammela T;  
PI WPI; 2005-182331/19.  
XX  
XX New heparin-binding Vascular Endothelial Growth Factor Receptor 3 ligands  
PT comprising prepro-VEGF-C, prepro-VEGF-D sequences or fragments, for  
PT treating neurodegenerative disorder, e.g. Alzheimer's, Parkinson's, or  
PT Huntington's disease.  
XX  
XX Disclosure; SEQ ID NO 63; 219pp; English.  
XX  
XX The invention relates to heparin-binding vascular endothelial growth  
CC factor receptor 3 (VEGFR-3) proteins and encoding polynucleotides. The  
CC heparin binding VEGFR-3 proteins are used for stimulating  
CC lymphangiogenesis or angiogenesis in a mammal, and for modulating the  
CC growth of mammalian endothelial cells, mammalian endothelial precursor  
CC cells or hematopoietic progenitor cells. The polypeptide may also be used  
CC for promoting recruitment, proliferation, differentiation, migration or  
CC survival of neuronal cells or neuronal precursor cells, and for treating  
CC neurodegenerative disorder, e.g. Alzheimer's disease, Parkinson's  
CC disease, Huntington's disease, motor neuron disease, Amyotrophic Lateral  
CC Sclerosis (ALS), dementia, or cerebral palsy. The present sequence  
CC represents human amphoterin.  
XX  
SQ Sequence 215 AA;  
Query Match 100.0%; Score 1149; DB 9; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.7e-93;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGKGDPKPRGKMSSVAFFVQTCREHHKKKHPPDASVNFSEFSKCSERWMTMSAKGKGF 60  
Db 1 MGKGDPKPRGKMSSVAFFVQTCREHHKKKHPPDASVNFSEFSKCSERWMTMSAKGKGF 60  
Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120  
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120  
Qy 121 SIGDVAKGLGEMWNNTAADKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKEK 180  
Db 121 SIGDVAKGLGEMWNNTAADKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKEK 180  
Qy 181 SKKKKEEEDDE 215  
Db 181 SKKKKEEEDDE 215

RESULT 13  
ADY14248  
ID ADY14248 standard; protein; 215 AA.  
XX  
XX ADY14248;  
AC  
XX 05-MAY-2005 (first entry)  
DT  
XX PRO polypeptide SEQ ID NO 54.  
DE  
XX  
XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;  
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
KW Antiallergic; ds; gene; diagnosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W02005016962-A2.  
PN  
XX  
XX 24-FEB-2005.  
PD  
XX  
XX 11-AUG-2004; 2004WO-US026249.  
PF  
XX  
XX 11-AUG-2003; 2003US-0493546P.  
PR  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX  
XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;  
PI WPI; 2005-182330/19.  
XX  
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
PT treating an immune related disorder, e.g. systemic lupus erythematosus,  
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.  
XX  
XX Claim 8; SEQ ID NO 54; 158pp; English.  
XX  
XX The invention relates to an isolated nucleic acid encoding a PRO  
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,  
CC composition, and method are useful for diagnosing and treating an immune  
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid  
CC arthritis. The present sequence represents a DNA encoding a PRO  
CC polypeptide.  
XX  
SQ Sequence 215 AA;  
Query Match 100.0%; Score 1149; DB 9; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.7e-93;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGKGDPKPRGKMSSVAFFVQTCREHHKKKHPPDASVNFSEFSKCSERWMTMSAKGKGF 60  
Db 1 MGKGDPKPRGKMSSVAFFVQTCREHHKKKHPPDASVNFSEFSKCSERWMTMSAKGKGF 60  
Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120  
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120  
Qy 121 SIGDVAKGLGEMWNNTAADKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKEK 180  
Db 121 SIGDVAKGLGEMWNNTAADKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKEK 180  
Qy 181 SKKKKEEEDDE 215  
Db 181 SKKKKEEEDDE 215

RESULT 14  
ADY85326  
ID ADY85326 standard; protein; 215 AA.



CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-  
CC binding fragment) binds to a vertebrate HMGB A box but does not  
CC specifically bind to non-A box epitopes of HMGB, and inhibits release of  
CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB  
CC protein. A method of treating a condition characterized by activation of  
CC an inflammatory cytokine cascade comprises administering an antibody of  
CC the invention, or its antigen-binding fragment. The condition is selected  
CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult  
CC respiratory distress syndrome, chronic obstructive pulmonary disease,  
CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,  
CC graft versus host disease, inflammatory bowel disease, multiple sclerosis  
CC and cachexia, especially sepsis, arthritis, or lupus. The present  
CC sequence is that of the A box of human HMGB1 ADY85012. An identical  
CC sequence is also found in rat and mouse HMGB1.

XX  
SQ Sequence 215 AA;

Query Match		100.0%;	Score 1149;	DB 9;	Length 215;
Best Local Similarity		100.0%;	Pred. No. 2.7e-93;		
Matches 215;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGKGDPPKPKGMSYAFFVOTCREEHKKHPDASVNFSEFSKCSERWKTMSAKEKGF	60		
Db	1	MGKGDPPKPKGMSYAFFVOTCREEHKKHPDASVNFSEFSKCSERWKTMSAKEKGF	60		
Qy	61	EDMAKADKARYEREMKTYIIPKGETKKKFKDPNAPKPPSAFFLCSEYRPKIKGEHPGL	120		
Db	61	EDMAKADKARYEREMKTYIIPKGETKKKFKDPNAPKPPSAFFLCSEYRPKIKGEHPGL	120		
Qy	121	SIGDVAKKLGMWNNTAADKQPYEKKAALKKEKYEKDIYAAYRAKGPDAAKKGVVKAEK	180		
Db	121	SIGDVAKKLGMWNNTAADKQPYEKKAALKKEKYEKDIYAAYRAKGPDAAKKGVVKAEK	180		
Qy	181	SKKKKEEEDDE	215		
Db	181	SKKKKEEEDDE	215		

Search completed: April 6, 2006, 10:19:12  
Job time : 263.97 secs







non-histone chromosomal high-mobility group 1 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I48688; A55402; I57021  
R;Yotov, W.V.; St-Arnaud, R.  
Nucleic Acids Res. 20, 3516, 1992  
A;Title: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mobility group 1 protein (HMG1).  
A;Reference number: I48687; MUID:92335012; PMID:1630928  
A;Accession: I48688  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-215 <RES>  
A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; EMBL:Z11997; NID:953381; PIDN:CAA56631.1; PI  
J. Ferrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.  
J. Biol. Chem. 269, 28803-28808, 1994  
A;Title: The mouse gene coding for high mobility group 1 protein (HMG1).  
A;Reference number: A55402; MUID:95050689; PMID:7961836  
A;Accession: A55402  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-189, 'E', 191-215 <FER>  
A;Cross-references: UNIPARC:UPI000016CDD6; EMBL:X80457; NID:9620097; PIDN:CAA56631.1; PI  
R;Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.  
Mamm. Genome 5, 91-99, 1994  
A;Title: Molecular cloning, expression analysis, and chromosomal localization of mouse HMG1.  
A;Reference number: I57021; MUID:94235965; PMID:8180479  
A;Accession: I57021  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-215 <R2>  
A;Cross-references: UNIPARC:UPI00000008A6; EMBL:U00431; NID:9437101; PIDN:AAA20508.1; PI  
C;Genetics:  
A;Gene: hmg1  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 99.4%; Score 1142; DB 2; Length 215;  
Best Local Similarity 99.1%; Pred. No. 2.4e-61;  
Matches 213; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSYAFFVQTCREHKKHPPDASVNFSEFSKCSERWKTMSAKGKGF 60  
Db 1 MGKGDPPKPRGKMSYAFFVQTCREHKKHPPDASVNFSEFSKCSERWKTMSAKGKGF 60

Qy 61 EDMAKADKARYEREMKTYIPPGKTKKKFDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120  
Db 61 EDMAKADKARYEREMKTYIPPGKTKKKFDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEMWNTAADDKQPYEKKAALKYKDYKDIAAYRAKGPDAAGKGVVKAKE 180  
Db 121 SIGDVAKKLGEMWNTAADDKQPYEKKAALKYKDYKDIAAYRAKGPDAAGKGVVKAKE 180

Qy 181 SKKKKEEEDDE 215  
Db 181 SKKKKEEEDDE 215

RESULT 5  
A28897  
nonhistone chromosomal protein HMG-1 - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C;Accession: A28897  
R;Tsuada, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.  
Biochemistry 27, 6159-6163, 1988  
A;Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide sequence  
A;Reference number: A28897; MUID:89050965; PMID:3191113  
A;Accession: A28897  
A;Molecule type: mRNA  
A;Residues: 1-215 <TSU>  
A;Cross-references: UNIPROT:P12682; UNIPARC:UPI000016C6C4; GB:M21683; GB:M21684; NID:g16

C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein; DNA binding; nucleus  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 99.2%; Score 1140; DB 2; Length 215;  
Best Local Similarity 99.1%; Pred. No. 3.2e-61;  
Matches 213; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSYAFFVQTCREHKKHPPDASVNFSEFSKCSERWKTMSAKGKGF 60  
Db 1 MGKGDPPKPRGKMSYAFFVQTCREHKKHPPDASVNFSEFSKCSERWKTMSAKGKGF 60

Qy 61 EDMAKADKARYEREMKTYIPPGKTKKKFDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120  
Db 61 EDMAKADKARYEREMKTYIPPGKTKKKFDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEMWNTAADDKQPYEKKAALKYKDYKDIAAYRAKGPDAAGKGVVKAKE 180  
Db 121 SIGDVAKKLGEMWNTAADDKQPYEKKAALKYKDYKDIAAYRAKGPDAAGKGVVKAKE 180

Qy 181 SKKKKEEEDDE 215  
Db 181 SKKKKEEEDDE 215

RESULT 6  
S29857  
nonhistone chromosomal protein HMG-1 - human  
C;Species: Homo sapiens (man)  
C;Date: 08-Dec-1993 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S29857  
R;Stros, M.; Dixon, G.H.  
Biochim. Biophys. Acta 1172, 231-235, 1993  
A;Title: A retroseudogene for non-histone chromosomal protein HMG-1.  
A;Reference number: S29857; MUID:93176821; PMID:8439568  
A;Accession: S29857  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-216 <STR>  
A;Cross-references: UNIPARC:UPI000011DFAA; EMBL:L08048; NID:g184250; PIDN:AAA64970.1; PI  
A;Note: the authors did not translate the codon for residue 1  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 97.7%; Score 1122.5; DB 2; Length 216;  
Best Local Similarity 96.6%; Pred. No. 3.5e-60;  
Matches 213; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MGKGDPPKPRGKMSYAFFVQTCREHKKHPPDASVNFSEFSKCSERWKTMSAKGKGF 60  
Db 1 MGKGDPPKPRGKMSYAFFVQTCREHKKHPPDASVNFSEFSKCSERWKTMSAKGKGF 60

Qy 61 EDMAKADKARYEREMKTYIPPGKTKKKFDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120  
Db 61 EDMAKADKARYEREMKTYIPPGKTKKKFDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEMWNTAADDKQPYEKKAALKYKDYKDIAAYRAKGPDAAGKGVVKAKE 180  
Db 121 SIGDVAKKLGEMWNTAADDKQPYEKKAALKYKDYKDIAAYRAKGPDAAGKGVVKAKE 180

Qy 181 SKKKKEEEDDE 215  
Db 181 SKKKKEEEDDE 216

RESULT 7  
S62355  
high mobility group protein 1 - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004





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C;Species: Salmo sp. (trout)
C;Date: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C;Accession: S48708
R;Stros, M.; Nishikawa, S.; Dixon, G.H.
Eur. J. Biochem. 225, 581-591, 1994
A;Title: cDNA sequence and structure of a gene encoding trout testis high-mobility-group
A;Reference numbers: S48708; MUID:95045507; PMID:7957172
A;Accession: S48708
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-204 <STR>
A;Cross-references: UNIPARC:UPI00001771D9
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;5-82/Domain: HMG box homology <HMG1>
F;91-165/Domain: HMG box homology <HMG2>

Query Match 72.3%; Score 837.5; DB 2; Length 204;
Best Local Similarity 71.8%; Pred. No. 2.8e-43;
Matches 150; Conservative 34; Mismatches 20; Indels 5; Gaps 2;

QY 1 MGKGDPPKPRGKMSSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGF 60
DB 1 MGK-DPRKPRGKMSSYAFFVQTCREHKKKHPASVNFSEFSKCSERWKTMSAKEKGF 59

QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPRPPSAFFLFCSEYRPKIKGEHPGL 120
DB 60 EDLAKLDKVREREMRSYIPPKGEKKRFPKNAPKRPSSAFFIFCADFRPQVKGETPGL 119

QY 121 SIGDVAKLGE MNNTAADKQPEYKKAALKKEKYEKDIAAYRAKGPDAAKKGVVKAEX 180
DB 120 SIGDVAKLGEKNLTAEDKVPYEKASKLKEKYEKDITAYRNKGKVPVS----MPAKA 175

QY 181 SKKKKEEEDDEDEDEDEDEDEDEDE 209
DB 176 AAPAKDDDDDDDDDDDDDDDDDDDDDEDEDE 204

RESULT 15
T01071
high mobility group protein T - rainbow trout
N;Alternate names: HMG-T protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01071
R;Pentecost, B.T.; Wright, J.M.; Dixon, G.H.
Nucleic Acids Res. 13, 4871-4888, 1985
A;Title: Isolation and sequence of cDNA clones coding for a member of the family of high
A;Reference number: A24019; MUID:85269614; PMID:4022777
A;Accession: T01071
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-204 <PEN>
A;Cross-references: UNIPROT:P07746; UNIPARC:UPI000012CA3E; EMBL:X02666; NID:g64327; PIDN
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;91-165/Domain: HMG box homology <HMG>

Query Match 72.3%; Score 830.5; DB 2; Length 204;
Best Local Similarity 71.3%; Pred. No. 7.3e-43;
Matches 149; Conservative 35; Mismatches 20; Indels 5; Gaps 2;

QY 1 MGKGDPPKPRGKMSSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGF 60
DB 1 MGK-DPRKPRGKMSSYAFFVQTCREHKKKHPASVNFSEFSKCSERWKTMSAKEKGF 59

QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPRPPSAFFLFCSEYRPKIKGEHPGL 120
DB 60 EDLAKLDKVREREMRSYIPPKGEKKRFPKNAPKRPSSAFFIFCADFRPQVKGETPGL 119

QY 121 SIGDVAKLGE MNNTAADKQPEYKKAALKKEKYEKDIAAYRAKGPDAAKKGVVKAEX 180
DB 120 SIGDVAKLGEKNLTAEDKVPYEKASKLKEKYEKDITAYRNKGKVPVS----MPAKA 175

QY 181 SKKKKEEEDDEDEDEDEDEDEDEDEDE 209
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Db 176 AAPAKDDDDDDDDDDDDDDDDDDDDDEDEDE 204

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Job time : 42.0197 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:13:48 ; Search time 253.898 Seconds  
(without alignments)  
597.439 Million cell updates/sec

Title: US-10-717-984-1

Perfect score: 1149

Sequence: 1 MGKGDPPKPRGKMSYAFFV.....DEEEDEDEDEDEDDDE 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

\* Pred. No. is the number of results predicted by chance to have a  
\* score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	215	2	Q5T7C3_HUMAN
2	1149	100.0	215	2	Q4R844_MACFA
3	1145	99.7	215	2	Q9QX40_SPALAX
4	1144	99.6	214	1	HMGI_CANFA
5	1144	99.6	214	1	HMGI_HUMAN
6	1142	99.4	215	2	Q9QW76_SPALAX
7	1142	99.4	215	2	Q548R9_RAT
8	1142	99.4	215	2	Q58EV5_MOUSE
9	1140	99.2	214	1	HMGI_BOVIN
10	1139	99.1	215	2	O88611_SPALAX
11	1138	99.0	215	2	O88612_SPALAX
12	1137	99.0	214	1	HMGI_MOUSE
13	1137	99.0	214	1	HMGI_RAT
14	1136	98.9	215	2	O6P202_MOUSE
15	1135	98.8	214	1	HMGI_PIG
16	1129	98.3	215	2	O14321_HUMAN
17	1125	97.9	215	2	O8B002_MOUSE
18	1067	92.9	215	2	O9YH06_CHICK
19	1061.5	92.4	214	2	O9PUK9_CHICK
20	1061	92.3	211	2	O9NQJ4_HUMAN
21	1050.5	91.4	211	1	HMGI_X_HUMAN
22	1025	89.2	192	2	O5T7C5_HUMAN
23	1005	87.5	211	2	O6P4N5_XENTR
24	1001	87.1	211	2	Q7S242_XENLA
25	996	86.7	206	2	O5BKQ1_MOUSE
26	984.5	85.7	210	2	O91596_XENLA
27	981.5	85.4	210	2	O6GN05_XENLA
28	969	84.3	181	2	O8BNM0_MOUSE
29	955	83.1	178	2	O8C7C4_MOUSE
30	948	82.5	180	1	HMGI_CRIGR
31	929	80.9	209	2	Q5U072_HUMAN

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RESULT 1
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ID Q5T7C3_HUMAN PRELIMINARY; PRT; 215 AA.
AC Q5T7C3;
DT 01-FEB-2005 (Tremblrel. 29, Created)
DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE High-mobility group box 1.
GN Name=HMGB1; ORFNames=RP11-550P23.1-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
ON NCBI_TaxID=9606;
RX [1]
RN NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL353648; CAIL5600.1; -; Genomic_DNA.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;

Query Match 100.0%; Score 1149; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.9e-59;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSYAFFVOTCREEHKKKHPDASVNFSEFSKCSRWKTSKKEGKGF 60
Db 1 MGKGDPPKPRGKMSYAFFVOTCREEHKKKHPDASVNFSEFSKCSRWKTSKKEGKGF 60

Qy 61 EDMAKADKARYEMKTYIPPKGETKKKFPDAPKPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEMKTYIPPKGETKKKFPDAPKPPSAFFLFCSEYRPKIKGEHPGL 120

Qy 121 SIGDVAKKLGEMWNNTAADKQPYEKAAKIKKEYEKDIAARYAKGPKDPAKKGWVKAEX 180
Db 121 SIGDVAKKLGEMWNNTAADKQPYEKAAKIKKEYEKDIAARYAKGPKDPAKKGWVKAEX 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 2
Q4R844_MACFA
ID Q4R844_MACFA PRELIMINARY; PRT; 215 AA.
AC Q4R844;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Testis cDNA clone: QtsA-13487, similar to human high-mobility group

```

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32 924 80.4 208 1 HM22_HUMAN
33 921.5 80.2 209 1 HM22_PIG
34 920.5 80.1 208 2 Q5U071_HUMAN
35 917.5 79.9 210 2 Q5FV00_RAT
36 914 79.5 209 1 HM22_MOUSE
37 912.5 79.4 209 1 HM22_RAT
38 910 79.2 206 1 HM22_CHICK
39 894.5 77.9 212 2 O8AVT3_XENLA
40 893 77.7 191 2 Q75MM1_HUMAN
41 892 77.6 212 2 Q7ZKX5_XENLA
42 885.5 77.1 205 2 Q7ZVC6_BRARE
43 884.5 77.0 212 2 Q6P7M9_XENTR
44 881.5 76.7 205 2 O6NX86_BRARE
45 873 76.0 212 2 Q91764_XENLA

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#### ALIGNMENTS

```

DE box 1 (HMGBl1);
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA International consortium for macaque cDNA sequencing, analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
RT Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB168615; BAE00728.1; -; mRNA.
SQ SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;

Query Match 100.0%; Score 1149; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.9e-59;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPKPKRGKMSVYAFFVQTCREHKKKHDPASVNFSEFSKCSERWMTSAKKGKF 60
Db 1 MGKGDPKPKRGKMSVYAFFVQTCREHKKKHDPASVNFSEFSKCSERWMTSAKKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEWNNNTAADKQPEKKAALKKYEKDIYAAYRAKGPDAAKKGWVKAKE 180
Db 121 SIGDVAKKLGEWNNNTAADKQPEKKAALKKYEKDIYAAYRAKGPDAAKKGWVKAKE 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

Query Match 100.0%; Score 1149; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.9e-59;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPKPKRGKMSVYAFFVQTCREHKKKHDPASVNFSEFSKCSERWMTSAKKGKF 60
Db 1 MGKGDPKPKRGKMSVYAFFVQTCREHKKKHDPASVNFSEFSKCSERWMTSAKKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEWNNNTAADKQPEKKAALKKYEKDIYAAYRAKGPDAAKKGWVKAKE 180
Db 121 SIGDVAKKLGEWNNNTAADKQPEKKAALKKYEKDIYAAYRAKGPDAAKKGWVKAKE 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 3
Q9QX40 SPAEH PRELIMINARY; PRT; 215 AA.
AC Q9QX40;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE High mobility group protein.
GN Name=HMG1;
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Spalacinae; Nannospalax.
OX NCBI_TaxID=30637;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee K.-L.D., Lum H.-K., Nevo E.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF078820; AAC27653.2; -; Genomic_DNA.
DR HSSP; P07156; INHN
DR SNR; Q9QX40; 2-84, 93-171.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; Highmobility_12.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.

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DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS01118; HMG_BOX_2; 2.
SQ SEQUENCE 215 AA; 24895 MW; 599FB8A6FDF41F17 CRC64;

Query Match 99.7%; Score 1145; DB 2; Length 215;
Best Local Similarity 99.5%; Pred. No. 1.2e-58;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPKPKRGKMSVYAFFVQTCREHKKKHDPASVNFSEFSKCSERWMTSAKKGKF 60
Db 1 MGKGDPKPKRGKMSVYAFFVQTCREHKKKHDPASVNFSEFSKCSERWMTSAKKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEWNNNTAADKQPEKKAALKKYEKDIYAAYRAKGPDAAKKGWVKAKE 180
Db 121 SIGDVAKKLGEWNNNTAADKQPEKKAALKKYEKDIYAAYRAKGPDAAKKGWVKAKE 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 4
HMG1 CANFA
ID HMG1 CANFA STANDARD; PRT; 214 AA.
AC Q9YKA4;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE High mobility group protein 1 (HMG-1) (High mobility group protein
DE B1).
GN Name=HMGBl;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
RX MEDLINE; 22932580; PubMed; 14571134; DOI=10.1159/000073415;
RA Murua Escobar H., Meyer B., Richter A., Becker K., Flohr A.M.,
RA Bullerdiek J., Nolte I.;
RT "Molecular characterization of the canine HMGBl.";
RL Cytogenet. Genome Res. 101:33-38(2003).
CC -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC double stranded DNA (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AV135519; AAN11296.1; -; mRNA.
DR EMBL; AV135521; AAN11319.1; -; Genomic_DNA.
DR HSSP; P07155; 1AAB.
DR SMR; Q9YKA4; 1-83, 92-170.
DR Ensembl; ENSCARG0000006597; Canis familiaris.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS01118; HMG_BOX_2; 2.
KW Chromosomal protein; DNA-binding; Nuclear protein; Repeat.
FT INIT_MET 0 By similarity.

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FT DNA_BIND 8 78 HMG box 1.
FT DNA_BIND 94 162 HMG box 2.
FT COMPBIAS 185 214 Asp/Glu-rich (acidic).
SQ SEQUENCE 214 AA; 24763 MW; B3C6A80FC7F0F433 CRC64;

Query Match 99.6%; Score 1144; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.3e-58;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 KGSDPKPRGQMSYAFVQTCREHKKKHPDASVNFSEPKKSKRWKNTSAKEKGF 61
Db 1 KGSDPKPRGQMSYAFVQTCREHKKKHPDASVNFSEPKKSKRWKNTSAKEKGF 60
Oy 62 DMAKADKARYEREMKTYIPPGKTKKPKDNAPKPPSAFLPCSEVRPKIKGEHPGLS 121
Db 61 DMAKADKARYEREMKTYIPPGKTKKPKDNAPKPPSAFLPCSEVRPKIKGEHPGLS 120
Oy 122 IGDVAKKLGEMWNTAADDKQPYEKKAALKKEKYEKIDIAAYRAKGPDAKKGVVVKAES 181
Db 121 IGDVAKKLGEMWNTAADDKQPYEKKAALKKEKYEKIDIAAYRAKGPDAKKGVVVKAES 180
Oy 182 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 214

RESULT 5
HMGI HUMAN
ID HMGI_HUMAN STANDARD; PRT; 214 AA.
AC P09429; O61BE1;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE High mobility group protein 1 (HMG-1) (High mobility group protein
DE B1).
GN Name=HMG1; Synonym=HMG1;
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RP MEDLINE=89160247; PubMed=2922262;
RA Wen L., Huang J.K., Johnson B.H., Reek G.R.;
RT "A human placental cDNA clone that encodes nonhistone chromosomal
RT protein HMG-1.";
RL Nucleic Acids Res. 17:1197-1214(1989).
[2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;
RA Ferrarini S., Finelli P., Rocchi M., Bianchi M.E.;
RT "The active gene that encodes human high mobility group 1 protein
RT (HMG1) contains introns and maps to chromosome 13.";
RL Genomics 35:367-371(1996).
[3]
RN NUCLEOTIDE SEQUENCE [MRNA].
RP He F.T., Yang Z.H., Ji Q., Li R., Peng J., Jiang Y., Zhong X.;
RT Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
[4]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP TISSUE=Small intestine;
RC The German cDNA consortium;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
[5]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
RT vector (pDONR201).";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
[6]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
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RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
[7]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain, Carvix, and Testis;
RX MEDLINE=42388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanches A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
RN PROTEIN SEQUENCE OF 57-64 AND 112-126.
RC TISSUE=Mammary carcinoma;
RX MEDLINE=97295304; PubMed=9150946;
RA Raemussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
RA Simpson R.J., Dorow D.S.;
RT "Two-dimensional electrophoretic analysis of human breast carcinoma
RT proteins: mapping of proteins that bind to the SH3 domain of mixed
RT lineage kinase MLK2.";
RL Electrophoresis 18:588-598(1997).
CC -1- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC double stranded DNA.
CC -1- INTERACTION:
CC P04637:TP53; NbExp=1; IntAct=EBI-389432, EBI-366083;
CC O15350:TP73; NbExp=1; IntAct=EBI-389432, EBI-389606;
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC -1- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X12597; CAA31110.1; -; mRNA.
DR EMBL; U51677; AAB08987.1; -; Genomic DNA.
DR EMBL; AY377859; AAQ91389.1; -; mRNA.
DR EMBL; CR749614; CAH18408.1; -; mRNA.
DR EMBL; CR456863; CAG33144.1; -; mRNA.
DR EMBL; BT006940; AAP35586.1; -; mRNA.
DR EMBL; BT020159; AAV38961.1; -; mRNA.
DR EMBL; BC003378; AAH03378.1; -; mRNA.
DR EMBL; BC030981; AAH30981.1; -; mRNA.
DR EMBL; BC066889; AAH66889.1; -; mRNA.
DR EMBL; BC067732; AAH67732.1; -; mRNA.
DR PIR; S02826; S02826.
DR HSP; P07156; INHN.
DR SMR; P09429; 1-83, 92-170.
DR IntAct; P09429; -.
DR EMBL; ENSG00000189403; Homo sapiens.
DR HGNC; HGNC:4983; HMG1.
DR H-InvDB; HIX0011209; -.
DR MIM; 163905; -.
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DR GO: 0000793; C: condensed chromosome; IDA.
DR GO: 0008301; F: DNA bending activity; TAS.
DR GO: 0008134; F: transcription factor binding; TAS.
DR GO: 0006288; P: base-excision repair, DNA ligation; IDA.
DR GO: 0006310; P: DNA recombination; TAS.
DR GO: 0006281; P: DNA repair; TAS.
DR GO: 0006268; P: DNA unwinding; NAS.
DR GO: 0006325; P: establishment and/or maintenance of chromatin. . ; TAS.
DR GO: 0017055; P: negative regulation of transcriptional prei. . ; IDA.
DR GO: 0006357; P: regulation of transcription from RNA polyme. . ; IDA.
DR InterPro: IPR000135; Highmobility_12.
DR InterPro: IPR000910; HMG_12_box.
DR Pfam: PF00505; HMG box; 2.
DR PRINTS: PR00886; HIGHMOBLTY12.
DR SMART: SM00398; HMG; 2.
DR PROSITE: PS00353; HMG_BOX_1; 1.
DR PROSITE: PS01118; HMG_BOX_2; 2.
SQ SEQUENCE 215 AA; 24822 MW; D20D659274B575B4 CRC64;

Query Match 99.4%; Score 1142; DB 2; Length 215;
Best Local Similarity 99.5%; Pred. No. 1.8e-58;
Matches 214; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGKGDPKKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWTKMSAKEKGKF 60
Db 1 MGKGDPKKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWTKMSAKEKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKFKDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKFKDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKIDIAAYRAKGPDAAKKGVVKAKE 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKIDIAAYRAKGPDAAKKGVVKAKE 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 7
Q548R9 RAT PRELIMINARY; PRT; 215 AA.
AC Q548R9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Amphoterin.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Ito T., Suzuki A., Horimoto N., Imai E., Hori M.;
RT "Amphoterin is associated with the development of the kidney.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275734; AAF82799.1; -; mRNA.
SQ SEQUENCE 215 AA; 24894 MW; 8A868DB266D552B5 CRC64;

Query Match 99.4%; Score 1142; DB 2; Length 215;
Best Local Similarity 99.1%; Pred. No. 1.8e-58;
Matches 213; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPKKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWTKMSAKEKGKF 60
Db 1 MGKGDPKKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWTKMSAKEKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKFKDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKFKDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKIDIAAYRAKGPDAAKKGVVKAKE 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKIDIAAYRAKGPDAAKKGVVKAKE 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 8
Q548R9 RAT PRELIMINARY; PRT; 215 AA.
AC Q548R9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Amphoterin.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Ito T., Suzuki A., Horimoto N., Imai E., Hori M.;
RT "Amphoterin is associated with the development of the kidney.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275734; AAF82799.1; -; mRNA.
SQ SEQUENCE 215 AA; 24894 MW; 8A868DB266D552B5 CRC64;

Query Match 99.4%; Score 1142; DB 2; Length 215;
Best Local Similarity 99.1%; Pred. No. 1.8e-58;
Matches 213; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPKKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWTKMSAKEKGKF 60
Db 1 MGKGDPKKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWTKMSAKEKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKFKDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKFKDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKIDIAAYRAKGPDAAKKGVVKAKE 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKIDIAAYRAKGPDAAKKGVVKAKE 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 8
Q548R9 RAT PRELIMINARY; PRT; 215 AA.
AC Q548R9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Amphoterin.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Ito T., Suzuki A., Horimoto N., Imai E., Hori M.;
RT "Amphoterin is associated with the development of the kidney.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275734; AAF82799.1; -; mRNA.
SQ SEQUENCE 215 AA; 24894 MW; 8A868DB266D552B5 CRC64;
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Q58EV5\_MOUSE  
ID Q58EV5\_MOUSE PRELIMINARY; PRT; 215 AA.  
AC Q58EV5;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation thymus)  
DE High mobility group box 1 (16 days neonate thymus cdna, RIKEN full-length enriched library, clone:A130064K11 product:high mobility group box 1, full insert sequence) (13 days embryo heart cdna, RIKEN full-length enriched library, clone:D330050N16 product:high mobility group box 1, full insert sequence).  
DN Name=Hmgbl;  
DN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Colon, and Mammary tumor. C3;  
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RG NIH MGC Project;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;  
RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Bono H., Baldarelli R., Barch G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brucic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierki R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Varadar R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Barney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).  
RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;  
RX MEDLINE=20530933; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).  
RN [9]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RA Adachi J., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirokawa T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CS7BL/6J; TISSUE=Heart;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hangsaku T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC091741; AAH91741.1; -; mRNA.  
DR EMBL; BC094030; AAH94030.1; -; mRNA.  
DR EMBL; AK037928; BAC29902.1; -; mRNA.  
DR EMBL; AK084841; BAC39289.1; -; mRNA.  
DR SMR; Q58EV5; 2-84, 93-171.  
DR MGI; MGI:196113; Hmgb1.  
DR GO; GO:0005615; C:extracellular space; IDA.  
DR GO; GO:0005634; C:nucleus; TAS.  
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.  
DR GO; GO:0006810; P:transport; IDA.  
DR InterPro; IPR000135; Highmobility\_12.  
DR InterPro; IPR000910; HMG\_12\_box.  
DR Pfam; PF00505; HMG\_box; 2.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS00353; HMG\_BOX\_1; 1.  
DR PROSITE; PS01118; HMG\_BOX\_2; 2.  
SQ SEQUENCE 215 AA; 24894 MW; 8A86DE26D552B5 CRC64;  
Query Match 99.4%; Score 1142; DB 2; Length 215;  
Best Local Similarity 99.1%; Pred. No. 1.8e-58;  
Matches 213; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKGDPPKPKGKSSVYAFVQTCREHKHKKHPDASVNFSEFSKCSERWKTMSAKGKGF 60  
DB 1 MGKGDPPKPKGKSSVYAFVQTCREHKHKKHPDASVNFSEFSKCSERWKTMSAKGKGF 60  
QY 61 EDNAKADKARYEMKTYIPPKGETKKKFKDPNAPKPPSAFLFCSEYRPKIKGHPGL 120  
DB 61 EDNAKADKARYEMKTYIPPKGETKKKFKDPNAPKPPSAFLFCSEYRPKIKGHPGL 120  
QY 121 SIGDVAKKLGEMNNNTAADKQYKKAALKKEKYKDI AAYRAKGPDAKKGWVKAEK 180  
DB 121 SIGDVAKKLGEMNNNTAADKQYKKAALKKEKYKDI AAYRAKGPDAKKGWVKAEK 180  
QY 181 SKKKKEEEDDE 215  
DB 181 SKKKKEEEDDE 215  
RESULT 9  
HMG1\_BOVIN STANDARD; PRT; 214 AA.  
ID AC P10103;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE High mobility group protein 1 (HMG-1) (High mobility group protein  
DE B1).

GN Name=HMG1; Synonyms=HMG1;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC STRAIN=Holstein; TISSUE=Petal thymus;  
RA MEDLINE=89057489; PubMed=3194213;  
RA Kaplan D.J., Duncan C.H.;  
RT "Full length cDNA sequence for bovine high mobility group 1 (HMG1)  
RT protein.";  
RN Nucleic Acids Res. 16:10375-10375(1988).  
[2]  
RP NUCLEOTIDE SEQUENCE [MRNA] OF 115-214.  
RX MEDLINE=84128872; PubMed=6141822;  
RA Pentecost B., Dixon G.H.;  
RT "Isolation and partial sequence of bovine cDNA clones for the high-  
RT mobility-group protein (HMG-1).";  
RN Biosci. Rep. 4:49-57(1984).  
[3]  
RP PROTEIN SEQUENCE OF 1-37; 45-156 AND 158-194.  
RX MEDLINE=81138848; PubMed=7202717; DOI=10.1016/0014-5793(80)80453-4;  
RA Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.;  
RT "The primary structures of non-histone chromosomal proteins HMG 1 and  
RT 2.";  
RN FEBS Lett. 122:264-270(1980).  
[4]  
RP PROTEIN SEQUENCE OF 1-36.  
RX MEDLINE=90306387; PubMed=2365081; DOI=10.1016/0014-5793(90)80308-6;  
RA Christen T., Bischoff M., Hobi R., Kuenzle C.C.;  
RT "High mobility group proteins 1 and 2 bind preferentially to  
RT brominated poly(dG-dC).poly(dG-dC) in the Z-DNA conformation but not  
RT to other types of Z-DNA.";  
RN FEBS Lett. 267:139-141(1990).  
CC -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds  
CC double stranded DNA.  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.  
CC -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC EMBL; X12796; CAA31284.1; -; mRNA.  
DR EMBL; M26110; AAA30567.1; -; mRNA.  
DR PIR; S01947; S01947.  
DR HSSP; P07156; LNHN.  
DR SMR; P10103; 1-83, 92-170.  
DR GO; GO:0000793; C:condensed chromosome; ISS.  
DR GO; GO:0008301; F:DNA bending activity; ISS.  
DR GO; GO:0005515; F:protein binding; ISS.  
DR GO; GO:0006288; P:base-excision repair; DNA ligation; ISS.  
DR GO; GO:0006310; P:DNA recombination; ISS.  
DR GO; GO:0006281; P:DNA repair; ISS.  
DR GO; GO:0006268; P:DNA unwinding; ISS.  
DR GO; GO:0006325; P:establishment and/or maintenance of chromatin; ISS.  
DR GO; GO:0017055; P:negative regulation of transcriptional preinitiation; ISS.  
DR InterPro; IPR000135; Highmobility\_12.  
DR InterPro; IPR000910; HMG\_12\_box.  
DR Pfam; PF00505; HMG\_box; 2.  
DR PRINTS; PR00886; HIGHMOBILITY12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS00353; HMG\_BOX\_1; 1.  
DR PROSITE; PS01118; HMG\_BOX\_2; 2.  
KW Chromosomal protein; Direct protein sequencing; DNA-binding;  
KW Nuclear protein; Repeat.  
DE INIT MET 0 0  
DE DNA\_BIND 8 78 HMG box 1.

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FT DNA BIND 94 162 HMG box 2.
FT COMEBIAS 185 214 Asp/Glu-rich (acidic).
FT CONFLICT 22 C -> S (in Ref. 3).
FT CONFLICT 105 105 C -> A (in Ref. 3).
FT CONFLICT 115 119 EHPGL -> PGGV (in Ref. 2).
FT CONFLICT 193 193 E -> D (in Ref. 3).
SQ SEQUENCE 214 AA; 24777 MW; B283A80FC7F0F433 CRC64;

Query Match 99.2%; Score 1140; DB 1; Length 214;
Best Local Similarity 99.5%; Pred. No. 2.3e-58;
Matches 213; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GKGDPKKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFKKCSERWKTMSAKEKGKF 61
Db 1 GKGDPKKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFKKCSERWKTMSAKEKGKF 60

Qy 62 DMAKADKARYEREMKTYIPPKGETKKKFPDAPKPPSAFFLFCSEYRPKIKGEHPGLS 121
Db 61 DMAKADKARYEREMKTYIPPKGETKKKFPDAPKPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy 122 IGDVAKKLGEMWNNTAADKQPYEKKAAKLEKEKDIYAAYRAKGPDAKGGVVKAEK 181
Db 121 IGDVAKKLGEMWNNTAADKQPYEKKAAKLEKEKDIYAAYRAKGPDAKGGVVKAEK 180

Qy 182 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 214

RESULT 10
O88611 SPAEH PRELIMINARY; PRT; 215 AA.
AC O88611;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE High mobility group protein.
GN Name=HMG1;
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Spalacinae; Nannospalax.
OX NCBI_TaxID=30637;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee K.-L.D., Lum H.-K., Nevo E.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF078817; AAC27650.2; -, Genomic_DNA.
DR HSSP; P07156; 1NHN.
DR SMR; O88611; 2-84, 93-171.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR00135; Highmobly_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBLTY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS0118; HMG_BOX_2; 2.
SQ SEQUENCE 215 AA; 24905 MW; 64816B6FCF6033EA CRC64;

[1]
Query Match 99.1%; Score 1139; DB 2; Length 215;
Best Local Similarity 99.1%; Pred. No. 2.6e-58;
Matches 213; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFKKCSERWKTMSAKEKGKF 60
Db 1 MGKGDPPKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFKKCSERWKTMSAKEKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDAPKPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDAPKPPSAFFLFCSEYRPKIKGEHPGL 120

Qy 121 IGDVAKKLGEMWNNTAADKQPYEKKAAKLEKEKDIYAAYRAKGPDAKGGVVKAEK 180
Db 121 IGDVAKKLGEMWNNTAADKQPYEKKAAKLEKEKDIYAAYRAKGPDAKGGVVKAEK 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 12
HMG1_MOUSE
ID HMG1_MOUSE STANDARD; PRT; 214 AA.
AC P63158; P07155; P27109; P27428;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE High mobility group protein 1 (HMG-1) (High mobility group protein
DE B1).

```

GN Name=Hmgbl; Synonyms=Hmg-1, Hmg1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C3H/He;  
RX MEDLINE=92335012; PubMed=1630928;  
RA Yotov W.V., St Arnaud R.;  
RT "Nucleotide sequence of a mouse cDNA encoding the nonhistone  
RT chromosomal high mobility group protein-1 (HMG1).";  
RL Nucleic Acids Res. 20:3516-3516(1992).  
RN [2]  
RP NUCLEOTIDE SEQUENCE  
RX MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;  
RA Pauken C.M., Nagle D.B., Bucan M., Lo C.W.;  
RT "Molecular cloning, expression analysis, and chromosomal localization  
RT of mouse Hmg1-containing sequences";  
RL Mamm. Genome 5:91-99(1994).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/Sv; TISSUE=Liver;  
RX MEDLINE=95050689; PubMed=7961836;  
RA Ferrari S., Ronfani L., Calogero S., Bianchi M.;  
RT "The mouse gene coding for high mobility group 1 protein (HMG1).";  
RL J. Biol. Chem. 269:28803-28808(1994).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=AKR/J;  
RA Ghosh B.;  
RT Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klatsch R.D., Collins R.S., Wagner K.H., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scaplenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Binds preferentially single-stranded DNA and unwinds  
CC double stranded DNA. Heparin-binding protein that has a role in  
CC the extension of neurite-type cytoplasmic processes in developing  
CC cells.  
CC -1- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated  
CC with the plasma membrane of filopodia in process-growing cells,  
CC and also deposited into the substrate-attached material.  
CC -1- SIMILARITY: Belongs to the HMG1/HMG2 protein family.  
CC -1- SIMILARITY: Contains 2 HMG box DNA-binding domains.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; Z11997; CAA78042.1; -; mRNA.

DR EMBL; U00431; AAA20508.1; -; mRNA.  
DR EMBL; X80457; CAA56631.1; -; Genomic DNA.  
DR EMBL; L38477; AAA57042.1; -; mRNA.  
DR EMBL; BC006586; AAH06586.1; -; mRNA.  
DR EMBL; BC008565; AAH08565.1; -; mRNA.  
DR EMBL; BC083067; AAH83067.1; -; mRNA.  
DR EMBL; BC085090; AAH85090.1; -; mRNA.  
DR PIR; I48688; I48688.  
DR SNR; P63158; 1-83, 92-170.  
DR MGI; MGI.96113; Hmgbl.  
DR GO; GO:0005615; C:extracellular space; IDA.  
DR GO; GO:0005634; C:nucleus; TAS.  
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.  
DR GO; GO:0006810; P:transport; IDA.  
DR InterPro; IPR000135; Highmobility\_12.  
DR InterPro; IPR000910; HMG\_12\_box.  
DR Pfam; PF00505; HMG\_box\_2.  
DR PRINTS; PR00886; HIGHMOBILITY12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS00353; HMG\_BOX\_1; 1.  
DR PROSITE; PS01118; HMG\_BOX\_2; 2.  
DR KEGG; K01118; HMG1; 1.  
KW Chromosomal protein; DNA-binding; Heparin-binding; Nuclear protein;  
KW Repeat.  
FT INIT MET 0 0 By similarity.  
FT DNA\_BIND 8 78 HMG box 1.  
FT DNA\_BIND 94 162 HMG box 2.  
FT COMPIAS 185 214 Asp/Glu-rich (acidic).  
FT CONFLICT 178 178 E -> V (in Ref. 4).  
FT CONFLICT 189 189 D -> E (in Ref. 3).  
SQ SEQUENCE 214 AA; 24763 MW; B3C6A91FD6F1B133 CRC64;  
Query Match 99.0%; Score 1137; DB 1; Length 214;  
Best Local Similarity 99.1%; Pred. No. 3.4e-58;  
Matches 212; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GKGDPPKPGKSSYAFFVQTCEEHKKHDPDASVNFSSFKCSERWKTMSAKEGKPE 61  
DB 1 GKGDPPKPGKSSYAFFVQTCEEHKKHDPDASVNFSSFKCSERWKTMSAKEGKPE 60  
QY 62 DMAKADKARYEREMKTYIPKGETKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGLS 121  
DB 61 DMAKADKARYEREMKTYIPKGETKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGLS 120  
QY 122 IGDVAKLKGEMWNTAADDKQPYEKKAALKKEKYEDIAAYRAKGPDAAKGVVKAEXS 191  
DB 121 IGDVAKLKGEMWNTAADDKQPYEKKAALKKEKYEDIAAYRAKGPDAAKGVVKAEXS 180  
QY 182 KKKKEEEDDE 215  
DB 181 KKKKEEEDDE 214  
RESULT 13  
HMG1 RAT  
ID HMG1 RAT STANDARD; PRT; 214 AA.  
AC P63159; P07155; P27109; P27428;  
DT 01-APR-1988 (Rel. 07, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE High mobility group protein 1 (HMG-1) (High mobility group protein B1)  
DE (Amphoterin) (Heparin-binding protein p30).  
GN Name=Hmgbl; Synonyms=Hmg-1, Hmg1;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=88067717; PubMed=3684582;



RA Paonessa G., Frank R., Cortese R.;  
RT "Nucleotide sequence of rat liver HMG1 cDNA.";  
RL Nucleic Acids Res. 15:9077-9077(1987).  
RN [2]  
RP SEQUENCE REVISION.  
RA Bianchi M.;  
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
RX MEDLINE=91358468; PubMed=1885601;  
RA Meremies J., Pihlakari R., Laitinen J., Wartiovaara J., Rauvala H.;  
RT "30-kDa heparin-binding protein of brain (amphoterin) involved in  
RT neurite outgrowth. Amino acid sequence and localization in the  
RT filopodia of the advancing plasma membrane.";  
RL J. Biol. Chem. 266:16722-16729(1991).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Kidney, Prostate, and Testis;  
RG NIH - Mammalian Gene Collection (MGC) project;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP PROTEIN SEQUENCE OF 1-20.  
RX MEDLINE=89066894; PubMed=2461949; DOI=10.1083/jcb.107.6.2293;  
RA Rauvala H., Meremies J., Pihlakari R., Korkalainen M., Huhtala M.L.,  
RA Panula P.;  
RT "The adhesive and neurite-promoting molecule p30: analysis of the  
RT amino-terminal sequence and production of antipeptide antibodies that  
RT detect p30 at the surface of neuroblastoma cells and of brain  
RT neurons";  
RL J. Cell Biol. 107:2293-2305(1988).  
RN [6]  
RP STRUCTURE BY NMR OF 87-164.  
RX MEDLINE=93233672; PubMed=8467791;  
RA Weir H.M., Kraulis P.J., Hill C.S., Raine A.R.C., Laue E.D.,  
RA Thomas J.O.;  
RT "Structure of the HMG box motif in the B-domain of HMG1.";  
RL ENBO J. 12:1311-1319(1993).  
RN [7]  
RP STRUCTURE BY NMR OF 1-83.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=96118376; PubMed=8527432;  
RA Hardman C.H., Broadhurst R.W., Raine A.R.C., Grasser K.D.,  
RA Thomas J.O., Laue E.D.;  
RT "Structure of the A-domain of HMG1 and its interaction with DNA as  
RT studied by heteronuclear three- and four-dimensional NMR  
RT spectroscopy";  
RL Biochemistry 34:16596-16607(1995).  
CC -I- FUNCTION: Binds preferentially single-stranded DNA and unwinds  
CC double stranded DNA. Heparin-binding protein that has a role in  
CC the extension of neurite-type cytoplasmic processes in developing  
CC cells.  
CC -I- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated  
CC with the plasma membrane of filopodia in process-growing cells,  
CC and also deposited into the substrate-attached material.  
CC -I- SIMILARITY: Belongs to the HMG1/HMG2 protein family.  
CC -I- SIMILARITY: Contains 2 HMG box DNA-binding domains.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; M64986; AAA40729.1; -; mRNA.  
DR EMBL; Y00463; CAA68526.1; -; mRNA.  
DR EMBL; BC061779; AAH61779.1; -; mRNA.  
DR EMBL; BC081839; AAH81839.1; -; mRNA.  
DR EMBL; BC088402; AAH88402.1; -; mRNA.  
DR PIR; A41175; NSRTH1.  
DR PDB; 1AAB; NMR; @=1-83.  
DR PDB; 1CKT; X-ray; A=7-77.  
DR PDB; 1HME; NMR; @=88-164.  
DR PDB; 1HMP; NMR; @=88-164.

DR SMR; P63159; 1-83, 92-170.  
DR Ensembl; ENSRNOG0000030351; Rattus norvegicus.  
DR RGD; 2802; Hmgbl.  
DR InterPro; IPR000135; Highmoblty\_12.  
DR InterPro; IPR000910; HMG\_12\_box.  
DR Pfam; PF00505; HMG box; 2.  
DR PRINTS; PR00886; HIGHMOBLTY12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS00353; HMG\_BOX\_1; 1.  
DR PROSITE; PS00118; HMG\_BOX\_2; 2.  
KW 3D-structure; Chromosomal protein; Direct protein sequencing;  
KW DNA-binding; Heparin-binding; Nuclear protein; Repeat.  
FT INIT MET 0  
FT DNA\_BIND 8 78 HMG box 1.  
FT DNA\_BIND 94 162 HMG box 2.  
FT COMBIAS 185 214 Asp/Glu-rich (acidic).  
FT HELIX 14 29  
FT TURN 31 32  
FT HELIX 37 49  
FT TURN 50 50  
FT TURN 53 55  
FT HELIX 57 74  
FT TURN 75 76  
FT HELIX 100 115  
FT TURN 117 118  
FT HELIX 121 134  
FT HELIX 137 158  
FT TURN 159 160  
SQ SEQUENCE 214 AA; 24763 MW; B3C6A91FD6F1B133 CRC64;  
Query Match 99.0%; Score 1137; DB 1; Length 214;  
Best Local Similarity 99.1%; Pred. No. 3.4e-58;  
Matches 212; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GKGDPPKPRGKMSYAFFVQTCREHKKHPDASVNFSEFSKCSERWKTMSAKEKGKFE 61  
DB 1 GKGDPPKPRGKMSYAFFVQTCREHKKHPDASVNFSEFSKCSERWKTMSAKEKGKFE 60  
QY 62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGEHPGLS 121  
DB 61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGEHPGLS 120  
QY 122 IGVAVKLGEMWNTAADKQPYEKAALKKEVKKDIAAYRAKGPDAAKGVVKAES 181  
DB 121 IGVAVKLGEMWNTAADKQPYEKAALKKEVKKDIAAYRAKGPDAAKGVVKAES 180  
QY 182 KKKKEDE 215  
DB 181 KKKKEDE 214  
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ID Q6P202 MOUSE PRELIMINARY; PRT; 215 AA.  
AC Q6P202; 2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hmgbl protein.  
GN Name=Hmgbl.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Wang J., Heide F.,



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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064790; AB464790.1; -; mRNA.
DR HSSP; P07155; IAA8.
DR SNR; O6P202; 2-84, 93-171.
DR MGI; MGI:96113; Hmgbl.
DR GO; GO:0005615; C:nucleus; TAS.
DR GO; GO:0005634; C:extracellular space; IDA.
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0006810; P:transport; IDA.
DR InterPro; IPR001135; Highmobility 12.
DR InterPro; IPR000910; HMG 12_box.
DR PRINTS; PR00505; HMG box; 2_box.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX 1; 1.
DR PROSITE; PS0118; HMG_BOX 2; 2.
SQ SEQUENCE 215 AA; 27920 MW; 7A998DEA7AB389D8 CRC64;

Query Match 98.8%; Score 1136; DB 2; Length 215;
Best Local Similarity 99.1%; Pred. No. 3.9e-58;
Matches 212; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGKGDPKKRGKSSVAFFVQTCREHHKKHPDASVNFSEFSKCSERWKTSAKEGKPF 60
Db 1 MGKGDPKKRGKSSVAFFVQTCREHHKKHPDASVNFSEFSKCSERWKTSAKEGKPF 60
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLCSEYRPKIKGHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLCSEYRPKIKGHPGL 120
QY 121 SIGDVAKKLGEWMNTAADKQPYEKKAAKLKEKYEKIDIAAYRAKGPDAAKGGVYKAEK 180
Db 121 SIGDVAKKLGEWMNTAADKQPYEKKAAKLKEKYEKIDIAAYRAKGPDAAKGGVYKAEK 180
QY 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

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AC F12682;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE High mobility group protein 1 (HMG-1) (High mobility group protein
DE B1).
GN Name=HMG1; Synonyms=HMG1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=89050965; PubMed=3191113;
RA Tsuda K.-I., Kikuchi M., Mori K., Waga S., Yoshida M.;
RT "Primary structure of non-histone protein HMG1 revealed by the
RT nucleotide sequence";
RL Biochemistry 27:6159-6163(1988).
CC -1- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC double stranded DNA.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC -1- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M21683; AAA31050.1; -; mRNA.
DR PIR; A28897; A28897.
DR HSSP; P07155; 1CKT.
DR SNR; P12682; 1-83, 92-170.
DR GO; GO:0000793; C:condensed chromosome; ISS.
DR GO; GO:0008301; F:DNA bending activity; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0006288; P:base-excision repair; DNA ligation; ISS.
DR GO; GO:0006310; P:DNA recombination; ISS.
DR GO; GO:0006281; P:DNA repair; ISS.
DR GO; GO:0006268; P:DNA unwinding; ISS.
DR GO; GO:0006325; P:negative regulation and/or maintenance of chromatin; ISS.
DR GO; GO:0017055; P:negative regulation of transcriptional preinitiation; ISS.
DR InterPro; IPR001135; Highmobility 12.
DR InterPro; IPR000910; HMG 12_box.
DR Pfam; PF00505; HMG box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX 1; 1.
DR PROSITE; PS0118; HMG_BOX 2; 2.
KW Chromosomal protein; DNA-binding; Nuclear protein; Repeat.
FT INIT MET 0 0 By similarity.
FT DNA_BIND 8 78 HMG box 1.
FT DNA_BIND 94 162 HMG box 2.
FT COMEBIAS 185 214 Asp/Glu-rich (acidic).
SQ SEQUENCE 214 AA; 24786 MW; B29C8A32D8D2C933 CRC64;

Query Match 98.8%; Score 1135; DB 1; Length 214;
Best Local Similarity 99.1%; Pred. No. 4.4e-58;
Matches 212; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GKGDPKKRGKSSVAFFVQTCREHHKKHPDASVNFSEFSKCSERWKTSAKEGKPF 61
Db 1 GKGDPKKRGKSSVAFFVQTCREHHKKHPDASVNFSEFSKCSERWKTSAKEGKPF 60
QY 62 DNMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLCSEYRPKIKGHPGLS 121
Db 62 DNMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLCSEYRPKIKGHPGLS 120
QY 122 IGDVAKKLGEWMNTAADKQPYEKKAAKLKEKYEKIDIAAYRAKGPDAAKGGVYKAEK 181
Db 122 IGDVAKKLGEWMNTAADKQPYEKKAAKLKEKYEKIDIAAYRAKGPDAAKGGVYKAEK 180
QY 182 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
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Job time : 253.898 secs
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

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288.890 Million cell updates/sec

Title: US-10-717-984-1

Perfect score: 1149

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgm2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgm2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgm2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 5: /cgm2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgm2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1144	99.6	214	2	US-09-214-881A-1
3	1140	99.2	214	2	US-09-214-881A-3
4	1135	98.8	214	2	US-09-214-881A-4
5	1128	98.2	214	2	US-09-214-881A-5
6	1056.5	91.9	213	2	US-09-949-016-10813
7	929	80.9	320	2	US-09-949-016-10728
8	924	80.4	208	2	US-09-538-092-1018
9	924	80.4	208	2	US-09-214-881A-2
10	921.5	80.2	209	2	US-09-214-881A-6
11	915.5	79.7	209	2	US-09-214-881A-8
12	900	78.3	206	2	US-09-214-881A-9
13	827	72.0	208	2	US-09-214-881A-11
14	824.5	71.8	879	2	US-09-914-259-38
15	809.5	70.5	201	2	US-09-214-881A-10
16	801	69.7	200	2	US-09-702-705-789
17	801	69.7	200	2	US-09-736-457-789
18	801	69.7	200	2	US-09-614-124B-789
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20	801	69.7	200	2	US-09-589-184-789
21	801	69.7	200	2	US-09-658-824-789
22	801	69.7	200	2	US-10-017-754-789
23	801	69.7	200	2	US-09-651-563-789
24	801	69.7	200	2	US-09-519-642-789
25	801	69.7	228	2	US-09-949-016-10496
26	796	69.3	207	2	US-09-702-705-1667
27	796	69.3	207	2	US-09-736-457-1667

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32	796	69.3	207	2	US-09-651-563-1667	Sequence 1667, Ap
33	796	69.3	207	2	US-09-702-705-324	Sequence 324, App
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35	789	68.7	200	2	US-09-614-124B-324	Sequence 324, App
36	789	68.7	200	2	US-09-671-325-324	Sequence 324, App
37	789	68.7	200	2	US-09-589-184-324	Sequence 324, App
38	789	68.7	200	2	US-09-658-824-324	Sequence 324, App
39	789	68.7	200	2	US-10-017-754-324	Sequence 324, App
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43	759.5	66.1	185	2	US-09-214-881A-7	Sequence 7, Appli
44	593	51.6	110	2	US-09-513-999C-4824	Sequence 4824, Ap
45	577	50.2	110	2	US-09-513-999C-4825	Sequence 4825, Ap

## ALIGNMENTS

### RESULT 1

US-09-538-092-883  
; Sequence 883, Application US/09538092  
; Patent NO. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CurapatSeqFormatter Version 0.9  
; SEQ ID NO 883  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (0)..(0)  
; OTHER INFORMATION: Polypeptide Accession Number P09429  
US-09-538-092-883

Qy	2	GKGDPPKPGKMSYAFVQTCEEHKKKHPDASVNFSEFSKCSERWKTMSAKEKGKPE	61
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Qy	62	DMAKADKARVEREMKTYIPPKGTCKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGLS	121
Db	61	DMAKADKARVEREMKTYIPPKGTCKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGLS	120
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Db	121	IGDVAKKLGEMWNTAADDKQPYEKKAALKKEYEKDIAAYRAKGPDAKKGYYVKAES	180
Qy	182	KKKKBEDE	215
Db	181	KKKKBEDE	214

### RESULT 2

US-09-214-881A-1



APPLICANT: Uesugi, Hiroko  
APPLICANT: Okazaki, Takahiro  
APPLICANT: Tanaka, Masao  
APPLICANT: Nakao, Kazuo  
APPLICANT: Yoshida, Michiteru  
APPLICANT: Shirakawa, Hitoshi  
APPLICANT: Osakada, Fumio  
TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES  
FILE REFERENCE: 068333.0104  
CURRENT APPLICATION NUMBER: US/09/214.881A  
CURRENT FILING DATE: 1999-06-07  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Rattus rattus  
US-09-214-881A-5

Query Match 98.2%; Score 1128; DB 2; Length 214;  
Best Local Similarity 98.1%; Pred. No. 7.5e-99;  
Matches 210; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 GKGDPKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGKF 61  
Db 1 GKGDPKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGKF 60  
Qy 62 DMAKADKARYEREMKTYIPPKGETKKPKDPNAPKPPSAFFLFCSEYRPKIKEHPGLS 121  
Db 61 DMAKADKARYEREMKTYIPPKGETKKPKDPNAPKPPSAFFLFCSEYRPKIKEHPGLS 120  
Qy 122 IGDVAKKLGEMWNTAADKQPYEKKAAKLEKEKDIAYRAKGPDAKKGVVYKAEK 181  
Db 121 IGDVAKKLGEMWNTAADKQPYEKKAAKLEKEKDIAYRAKGPDAKKGVVYKAEK 180  
Qy 182 KKKKEEEDDE 215  
Db 181 KKKKEEEDDE 214

RESULT 6  
US-09-949-016-10813  
Sequence 10813, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949.016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10813  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-10813

Query Match 91.9%; Score 1056.5; DB 2; Length 213;  
Best Local Similarity 94.8%; Pred. No. 4.2e-92;  
Matches 201; Conservative 3; Mismatches 7; Indels 1; Gaps 1;  
Qy 1 MGKDPKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGKF 60  
Db 3 MGKDPKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGKF 62

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKEHPGL 120  
Db 63 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKEHPGL 122  
Qy 121 SIGDVAKKLGEMWNTAADKQPYEKKAAKLEKEKDIAYRAKGPDAKKGVVYKAEK 180  
Db 123 SIGDVAKKLGEMWNTAADKQPYEKKAAKLEKEKDIAYRAKGPDAKKGVVYKAEK 182  
Qy 181 SKKKKEEEDDE 212  
Db 183 SKKKKEEEDDE 213

RESULT 7  
US-09-949-016-10728  
Sequence 10728, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949.016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10728  
LENGTH: 320  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-10728

Query Match 80.9%; Score 929; DB 2; Length 320;  
Best Local Similarity 81.3%; Pred. No. 7.7e-80;  
Matches 170; Conservative 19; Mismatches 20; Indels 0; Gaps 0;  
Qy 1 MGKDPKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGKF 60  
Db 112 MGKDPKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGKF 171  
Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKEHPGL 120  
Db 172 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKEHPGL 231  
Qy 121 SIGDVAKKLGEMWNTAADKQPYEKKAAKLEKEKDIAYRAKGPDAKKGVVYKAEK 180  
Db 232 SIGDTAKKLGEMWSEQSAKDKQPYEKKAAKLEKEKDIAYRAKGPDAKKGVVYKAEK 291  
Qy 181 SKKKKEEEDDE 209  
Db 292 SKKKKEEEDDE 320

RESULT 8  
US-09-538-092-1018  
Sequence 1018, Application US/09538092  
Patent No. 6753314  
GENERAL INFORMATION:  
APPLICANT: Giot, Loic  
APPLICANT: Mansfield, Traci A.  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542  
CURRENT APPLICATION NUMBER: US/09/538.092  
CURRENT FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 60/127,352  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/178,965

```
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqformatter Version 0.9
; SEQ ID NO 1018
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018

Query Match      80.4%; Score 924; DB 2; Length 208;
Best Local Similarity 81.2%; Pred. No. 1.4e-79;
Matches 169; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

Qy  2 GKGDPPKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGF 61
Db  1 GKGDPNKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGF 60
Qy  62 DMAKADKARYEREMKTYIPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGLS 121
Db  61 DMAKSDKARYDREMNKTVPPKGGKKKKDPNAPKPPSAFFLFCSEHRPKIKSEHPGLS 120
Qy  122 IGDVAKKLGEMWNNTAADKKQPYEKAAKLKEKYKDIAAYRAKGPDAAKGVVKAES 181
Db  121 IGD TAKKLGEMWSEQSAKDKQPYEQAAKLKEKYKDIAAYRAKGSEAGKGGPRPTGS 180
Qy  182 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 209
Db  181 KKKNEPEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 208

RESULT 9
US-09-214-881A-2
; Sequence 2, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-2

Query Match      80.4%; Score 924; DB 2; Length 208;
Best Local Similarity 81.2%; Pred. No. 1.4e-79;
Matches 169; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

Qy  2 GKGDPPKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGF 61
Db  1 GKGDPNKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGF 60
Qy  62 DMAKADKARYEREMKTYIPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGLS 121
Db  61 DMAKSDKARYDREMNKTVPPKGGKKKKDPNAPKPPSAFFLFCSEHRPKIKSEHPGLS 120
Qy  122 IGDVAKKLGEMWNNTAADKKQPYEKAAKLKEKYKDIAAYRAKGPDAAKGVVKAES 181
Db  121 IGD TAKKLGEMWSEQSAKDKQPYEQAAKLKEKYKDIAAYRAKGSEAGKGGPRPTGS 180
Qy  182 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 209
Db  181 KKKNEPEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 208

RESULT 10
US-09-214-881A-6
; Sequence 6, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-214-881A-6

Query Match      80.2%; Score 921.5; DB 2; Length 209;
Best Local Similarity 81.4%; Pred. No. 2.3e-79;
Matches 171; Conservative 18; Mismatches 20; Indels 1; Gaps 1;

Qy  2 GKGDPPKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGF 61
Db  1 GKGDPNKPRGKMSYAFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGF 60
Qy  62 DMAKADKARYEREMKTYIPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGLS 121
Db  61 DMAKSDKARYDREMNKTVPPKGGKKKKDPNAPKPPSAFFLFCSEHRPKIKSEHPGLS 120
Qy  122 IGDVAKKLGEMWNNTAADKKQPYEKAAKLKEKYKDIAAYRAKGPDAAKGVVKAES 181
Db  121 IGD TAKKLGEMWSEQSAKDKQPYEQAAKLKEKYKDIAAYRAKGSEAGKGGPRPTGS 180
Qy  182 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 211
Db  181 KKKNEPEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 209

RESULT 11
US-09-214-881A-8
; Sequence 8, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-214-881A-8

Query Match      79.7%; Score 915.5; DB 2; Length 209;
Best Local Similarity 80.5%; Pred. No. 8.6e-79;
Matches 169; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

Qy  2  GKGDPKPRGKMSYAFFVOTCREHHKKHDPDASVNFSEFSKCSERWKTMSAKEKGKFE 61
Db  1  GKGDPNPKRGKMSYAFFVOTCREHHKKHDPDASVNFSEFSKCSERWKTMSAKEKGKFE 60

Qy  62  DMAKADKARYEREMKTYIPPKGETTKKKFDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 121
Db  61  DMAKSDKARYDREMNVTVPKGGKKGKDPNAPKRPSPSAFFLFCSEHRRPKIKSEHPGLS 120

Qy  122  IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEYEKDIAAYRAKGPDAAKKGVVKAES 181
Db  121  IGD TAKKLGEMWSEQSAKDQPYEQKAAKLKEYEKDIAAYRAKGPDAAKKGVVKAES 180

Qy  182  KKKKEEEDDEDEDEDEDEDEED 211
Db  181  -KKNEPEDEEEDDEDEDEDEDEDE 209

RESULT 12
US-09-214-881A-9
; Sequence 9, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Okakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214.881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-214-881A-9

Query Match      78.3%; Score 900; DB 2; Length 206;
Best Local Similarity 80.1%; Pred. No. 2.5e-77;
Matches 165; Conservative 18; Mismatches 23; Indels 0; Gaps 0;

Qy  2  GKGDPKPRGKMSYAFFVOTCREHHKKHDPDASVNFSEFSKCSERWKTMSAKEKGKFE 61
Db  1  GKGDPNPKRGKMSYAFFVOTCREHHKKHDPDASVNFSEFSKCSERWKTMSAKEKGKFE 60

Qy  62  DMAKADKARYEREMKTYIPPKGETTKKKFDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 121
Db  61  EMAKGDARYDREMNVTVPKGGKKGKDPNAPKRPSPSAFFLFCSEHRRPKIKNDHPGLS 120

Qy  122  IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEYEKDIAAYRAKGPDAAKKGVVKAES 181
Db  121  IGD TAKKLGEMWSEQSAKDQPYEQKAAKLKEYEKDIAAYRAKGPDAAKKGVVKAES 180

Qy  182  KKKKEEEDDEDEDEDEDEDEED 207
Db  181  -KKNEPEDEEEDDEDEDEDEDEDE 207

; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-214-881A-8

Query Match      79.7%; Score 915.5; DB 2; Length 209;
Best Local Similarity 80.5%; Pred. No. 8.6e-79;
Matches 169; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

Qy  2  GKGDPKPRGKMSYAFFVOTCREHHKKHDPDASVNFSEFSKCSERWKTMSAKEKGKFE 61
Db  1  GKGDPNPKRGKMSYAFFVOTCREHHKKHDPDASVNFSEFSKCSERWKTMSAKEKGKFE 60

Qy  62  DMAKADKARYEREMKTYIPPKGETTKKKFDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 121
Db  61  DMAKSDKARYDREMNVTVPKGGKKGKDPNAPKRPSPSAFFLFCSEHRRPKIKSEHPGLS 120

Qy  122  IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEYEKDIAAYRAKGPDAAKKGVVKAES 181
Db  121  IGD TAKKLGEMWSEQSAKDQPYEQKAAKLKEYEKDIAAYRAKGPDAAKKGVVKAES 180

Qy  182  KKKKEEEDDEDEDEDEDEDEED 211
Db  181  -KKNEPEDEEEDDEDEDEDEDEDE 209

RESULT 13
US-09-214-881A-11
; Sequence 11, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Okakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214.881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-214-881A-11

Query Match      72.0%; Score 827; DB 2; Length 208;
Best Local Similarity 74.0%; Pred. No. 2e-70;
Matches 154; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

Qy  2  GKGDPKPRGKMSYAFFVOTCREHHKKHDPDASVNFSEFSKCSERWKTMSAKEKGKFE 61
Db  1  GKGDPKPRGKMSYAFFVOTCREHHKKHDPDASVNFSEFSKCSERWKTMSAKEKGKFE 60

Qy  62  DMAKADKARYEREMKTYIPPKGETTKKKFDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 121
Db  61  DLAKSDKACYREMNVTVPKGGKKGKDPNAPKRPSPSAFFLFCSEHRRPKIKIEYPGLS 120

Qy  122  IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEYEKDIAAYRAKGPDAAKKGVVKAES 181
Db  121  IGD TAKKLGEMWSEQSAKDQPYEQKAAKLKEYEKDIAAYRAKGPDAAKKGVVKAES 180

Qy  182  KKKKEEEDDEDEDEDEDEDEED 209
Db  181  KKKNDSEDEEEDDEDEDEDEDEED 208

RESULT 14
US-09-914-259-38
; Sequence 38, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914.259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-38

Query Match      71.8%; Score 824.5; DB 2; Length 879;
Best Local Similarity 85.4%; Pred. No. 1.9e-69;
Matches 158; Conservative 9; Mismatches 17; Indels 1; Gaps 1;
```







```
; APPLICANT: Tracey, Kevin J.
; APPLICANT: Yang, Huan
; APPLICANT: Warren Jr., Howland Shaw
; APPLICANT: Fink, Mitchell P.
; TITLE OF INVENTION: Use of HMG Fragments as
; TITLE OF INVENTION: Anti-Inflammatory Agents
; FILE REFERENCE: 3268.1001-001
; CURRENT APPLICATION NUMBER: US/10/147,447
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-147-447-1

Query Match      100.0%; Score 1149; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.6e-70;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKGDPKPKRGKMSSYAFFVQTCREHHKKKHPDASVNFSEFSKKCSERWKTMSAKGKGF 60
DB 1 MGKGDPKPKRGKMSSYAFFVQTCREHHKKKHPDASVNFSEFSKKCSERWKTMSAKGKGF 60
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKGHPGL 120
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKGHPGL 120
QY 121 SIGDVAKLGEWMNNTAADKQPYEKKAAKLKYEKDIYAAYRAKGPDAAKKGVVKAEK 180
DB 121 SIGDVAKLGEWMNNTAADKQPYEKKAAKLKYEKDIYAAYRAKGPDAAKKGVVKAEK 180
QY 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
DB 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 4
US-10-456-949-1
; Sequence 1, Application US/10456949
; Publication No. US2004005316A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3268.1001-006
; CURRENT APPLICATION NUMBER: US/10/456,949
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-456-949-1

Query Match      100.0%; Score 1149; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.6e-70;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKGDPKPKRGKMSSYAFFVQTCREHHKKKHPDASVNFSEFSKKCSERWKTMSAKGKGF 60
DB 1 MGKGDPKPKRGKMSSYAFFVQTCREHHKKKHPDASVNFSEFSKKCSERWKTMSAKGKGF 60
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKGHPGL 120
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKGHPGL 120
QY 121 SIGDVAKLGEWMNNTAADKQPYEKKAAKLKYEKDIYAAYRAKGPDAAKKGVVKAEK 180
DB 121 SIGDVAKLGEWMNNTAADKQPYEKKAAKLKYEKDIYAAYRAKGPDAAKKGVVKAEK 180
QY 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
DB 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 5
US-10-456-947-1
; Sequence 1, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMBG POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456,947
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147,447
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Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGHPGL 120
Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKE 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKE 180
Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 9
US-10-868-549-22
; Sequence 22, Application US/10868549
; Publication No. US20050043235A1
; GENERAL INFORMATION:
; APPLICANT: Alitalia et al.
; TITLE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY
; FILE REFERENCE: 28967/39117A
; CURRENT APPLICATION NUMBER: US/10/868,549
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,114
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-549-22

Query Match 100.0%; Score 1149; DB 5; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.6e-70;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHDPASVNFSEFSKKCSERWKTMSAKGKGF 60
Db 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHDPASVNFSEFSKKCSERWKTMSAKGKGF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKE 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKE 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 11
US-10-938-992-38
; Sequence 38, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-938-992-38

Query Match 99.7%; Score 1145; DB 5; Length 215;
Best Local Similarity 99.5%; Pred. No. 6.7e-70;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHDPASVNFSEFSKKCSERWKTMSAKGKGF 60
Db 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHDPASVNFSEFSKKCSERWKTMSAKGKGF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKE 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKE 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 12
US-09-214-881A-1
; Sequence 1, Application US/09214881A
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; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-992-74

Query Match 100.0%; Score 1149; DB 5; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.6e-70;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHDPASVNFSEFSKKCSERWKTMSAKGKGF 60
Db 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHDPASVNFSEFSKKCSERWKTMSAKGKGF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKE 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKE 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 11
US-10-938-992-38
; Sequence 38, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-938-992-38

Query Match 99.7%; Score 1145; DB 5; Length 215;
Best Local Similarity 99.5%; Pred. No. 6.7e-70;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHDPASVNFSEFSKKCSERWKTMSAKGKGF 60
Db 1 MGKGDPPKPRGKMSSYAFFVQTCREHHKKHDPASVNFSEFSKKCSERWKTMSAKGKGF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGHPGL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKE 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKKGVVKAKE 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 12
US-09-214-881A-1
; Sequence 1, Application US/09214881A
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; Patent No. US20020009749A1
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-1

Query Match 99.6%; Score 1144; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 7.8e-70;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GKGDPPKPRGMSYAFFVQTCREHKKKHPDASVNFSEFSKKCSERWTKMSAKEKGKFE 61
Db 1 GKGDPPKPRGMSYAFFVQTCREHKKKHPDASVNFSEFSKKCSERWTKMSAKEKGKFE 60
Qy 62 DMAKADKARYEREMKTYIPPKGETKKKFPDNPAPRPPSAFFLFCSEYRPKIKGEHPGLS 121
Db 61 DMAKADKARYEREMKTYIPPKGETKKKFPDNPAPRPPSAFFLFCSEYRPKIKGEHPGLS 120
Qy 122 IGDVAKKLGEMWNNTAADKQPYEKKAAKLEKYEKDI AAYRAKGPDAKKGVVKAES 181
Db 121 IGDVAKKLGEMWNNTAADKQPYEKKAAKLEKYEKDI AAYRAKGPDAKKGVVKAES 180
Qy 182 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 214

RESULT 14
US-10-938-992-40
; Sequence 40, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rec-HMGB1-His6
US-10-938-992-40

Query Match 99.6%; Score 1144; DB 5; Length 221;
Best Local Similarity 100.0%; Pred. No. 8e-70;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GKGDPPKPRGMSYAFFVQTCREHKKKHPDASVNFSEFSKKCSERWTKMSAKEKGKFE 61
Db 8 GKGDPPKPRGMSYAFFVQTCREHKKKHPDASVNFSEFSKKCSERWTKMSAKEKGKFE 67
Qy 62 DMAKADKARYEREMKTYIPPKGETKKKFPDNPAPRPPSAFFLFCSEYRPKIKGEHPGLS 121
Db 68 DMAKADKARYEREMKTYIPPKGETKKKFPDNPAPRPPSAFFLFCSEYRPKIKGEHPGLS 127
Qy 122 IGDVAKKLGEMWNNTAADKQPYEKKAAKLEKYEKDI AAYRAKGPDAKKGVVKAES 181
Db 128 IGDVAKKLGEMWNNTAADKQPYEKKAAKLEKYEKDI AAYRAKGPDAKKGVVKAES 187
Qy 182 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 188 KKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 221

RESULT 15
US-10-147-447-2
; Sequence 2, Application US/10147447
; Publication No. US20030060410A1
; GENERAL INFORMATION:
; APPLICANT: Tracey, Kevin J.
; APPLICANT: Yang, Huan

Query Match 99.6%; Score 1144; DB 5; Length 214;
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; APPLICANT: Warren Jr., Howland Shaw
; APPLICANT: Fink, Mitchell P.
; TITLE OF INVENTION: Use of HMG Fragments as
; TITLE OF INVENTION: Anti-Inflammatory Agents
; FILE REFERENCE: 3268.1001-001
; CURRENT APPLICATION NUMBER: US/10/147,447
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-147-447-2

Query Match          99.4%; Score 1142; DB 4; Length 215;
Best Local Similarity 99.1%; Pred. No. 1.le-69;
Matches 213; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MGKGDPPKPKGKSSYAFFVOTCREEHKKKHPDASVNFSEFSKCSERWKTMSAKGKF 60
Db      1 MGKGDPPKPKGKSSYAFFVOTCREEHKKKHPDASVNFSEFSKCSERWKTMSAKGKF 60

Qy      61 EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKRPPSAFFLCSEYRPKIKGEHPGL 120
Db      61 EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKRPPSAFFLCSEYRPKIKGEHPGL 120

Qy      121 SIGDVAKKLGEMWNNTAADKQPYEKKAALKKEKYEKDI AAYRAKGPDAAKKGVVKAEK 180
Db      121 SIGDVAKKLGEMWNNTAADKQPYEKKAALKKEKYEKDI AAYRAKGPDAAKKGVVKAEK 180

Qy      181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db      181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

Search completed: April 6, 2006, 10:32:46
Job time : 204.391 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:28:08 ; Search time 26.875 Seconds  
(without alignments)  
249.536 Million cell updates/sec

Title: US-10-717-984-1  
Perfect score: 1149  
Sequence: 1 MGKGDPPKPRGKMSYAFFV.....DEEEDEDEDEDEDDDE 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : 1: /SIDSS5/ptodata/2/pubpaa/US08 NEW PUB pep.\*  
2: /SIDSS5/ptodata/2/pubpaa/US06 NEW PUB pep.\*  
3: /SIDSS5/ptodata/2/pubpaa/US07 NEW PUB pep.\*  
4: /SIDSS5/ptodata/2/pubpaa/PCT NEW PUB pep.\*  
5: /SIDSS5/ptodata/2/pubpaa/US09 NEW PUB pep.\*  
6: /SIDSS5/ptodata/2/pubpaa/US10 NEW PUB pep.\*  
7: /SIDSS5/ptodata/2/pubpaa/US11 NEW PUB pep.\*  
8: /SIDSS5/ptodata/2/pubpaa/US60 NEW PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	215	6	US-10-821-234-1443
2	1149	100.0	215	7	US-11-186-422-11
3	1142	99.4	215	7	US-11-186-422-12
4	824.5	71.8	879	7	US-11-169-041-192
5	681	59.3	169	6	US-10-821-234-1234
6	370	32.2	69	7	US-11-186-422-14
7	287	25.0	54	6	US-10-719-150-6
8	287	25.0	54	7	US-11-186-422-13
9	278.5	24.2	502	7	US-11-087-099-8879
10	273	23.8	146	7	US-11-172-740-1569
11	268	23.3	141	7	US-11-087-099-3073
12	267.5	23.3	149	7	US-11-087-099-3510
13	267.5	23.3	149	7	US-11-172-740-1571
14	267.5	23.3	160	7	US-11-087-099-1105
15	263.5	22.9	142	7	US-11-087-099-4976
16	259	22.5	154	7	US-11-087-099-2474
17	259	22.5	154	7	US-11-172-740-1570
18	253.5	22.1	372	7	US-11-087-099-6977
19	251	21.8	388	7	US-11-087-099-4330
20	250.5	21.8	145	7	US-11-172-740-1572
21	250	21.8	446	7	US-11-087-099-370
22	248	21.6	152	7	US-11-087-099-313
23	248	21.6	152	7	US-11-172-740-1566
24	247	21.5	141	7	US-11-087-099-9185
25	247	21.5	487	7	US-11-087-099-11126

26	242	21.1	152	7	US-11-172-740-1565	Sequence 1565, Ap
27	240.5	20.9	380	7	US-11-087-099-5374	Sequence 5374, Ap
28	239	20.8	187	7	US-11-096-568A-32735	Sequence 32735, A
29	239	20.8	241	7	US-11-096-568A-32734	Sequence 32734, A
30	239	20.8	257	7	US-11-096-568A-32733	Sequence 32733, A
31	233	20.3	139	7	US-11-096-568A-13611	Sequence 13611, A
32	229.5	20.0	139	7	US-11-096-568A-26884	Sequence 26884, A
33	229.5	20.0	187	7	US-11-096-568A-26883	Sequence 26883, A
34	227.5	19.8	140	7	US-11-172-740-1564	Sequence 1564, Ap
35	220	19.1	164	7	US-11-096-568A-3510	Sequence 3510, Ap
36	218.5	19.0	234	7	US-11-096-568A-21031	Sequence 21031, A
37	216.5	18.8	165	7	US-11-096-568A-21033	Sequence 21033, A
38	216.5	18.8	212	7	US-11-096-568A-21032	Sequence 21032, A
39	212.5	18.5	137	7	US-11-096-568A-3511	Sequence 3511, Ap
40	209	18.2	124	7	US-11-096-568A-9681	Sequence 9681, Ap
41	209	18.2	162	7	US-11-096-568A-9680	Sequence 9680, Ap
42	206	17.9	93	7	US-11-087-099-869	Sequence 869, App
43	205	17.8	93	7	US-11-087-099-9518	Sequence 9518, Ap
44	202.5	17.6	92	7	US-11-087-099-8838	Sequence 8838, Ap
45	202.5	17.6	487	7	US-11-124-368A-308	Sequence 308, App

## ALIGNMENTS

RESULT 1  
US-10-821-234-1443  
; Sequence 1443, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1443  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1443

Query Match	100.0%;	Score 1149;	DB 6;	Length 215;
Best Local Similarity	100.0%;	Pred. No. 2.7e-77;		
Matches 215;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGKGDPPKPRGKMSYAFFVQTCREHHKHPDASVNFSEFSKCSERWTKMSAKEGKF	60	
Db	1	MGKGDPPKPRGKMSYAFFVQTCREHHKHPDASVNFSEFSKCSERWTKMSAKEGKF	60	
QY	61	EDMAKADKARYEREMKTYIPPKGETKKKPKDPNAPKPPSAFFLCSEYRPKINGEHPGL	120	
Db	61	EDMAKADKARYEREMKTYIPPKGETKKKPKDPNAPKPPSAFFLCSEYRPKINGEHPGL	120	
QY	121	SIGDVAKLGGEMWNTAADKQPYEKAALKKEKYEKDIAAYRAKGPDAKKGWVKAEK	180	
Db	121	SIGDVAKLGGEMWNTAADKQPYEKAALKKEKYEKDIAAYRAKGPDAKKGWVKAEK	180	
QY	181	SKKKKEEEDDE	215	
Db	181	SKKKKEEEDDE	215	

RESULT 2  
US-11-186-422-11  
; Sequence 11, Application US/11186422  
; Publication No. US20060057679A1



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; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; PRIOR FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-11

Query Match      100.0%; Score 1149; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 2,7e-77;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKGDPPKPRGMSSVAFFVQTCREHHKKHPDASVNFSEFSKCCSERWKTMSAKEKGKF 60
DB 1 MGKGDPPKPRGMSSVAFFVQTCREHHKKHPDASVNFSEFSKCCSERWKTMSAKEKGKF 60
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKPKDPNAPRPPSAFFLFCSEYRPKIKGHPGL 120
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKPKDPNAPRPPSAFFLFCSEYRPKIKGHPGL 120
QY 121 SIGDVAKLGEWNNNTAADKQPYEKKAAKLEKYEKIDIAAYRAKGPDAAKKGVVKAEK 180
DB 121 SIGDVAKLGEWNNNTAADKQPYEKKAAKLEKYEKIDIAAYRAKGPDAAKKGVVKAEK 180
QY 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
DB 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKPKDPNAPRPPSAFFLFCSEYRPKIKGHPGL 120
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKPKDPNAPRPPSAFFLFCSEYRPKIKGHPGL 120
QY 121 SIGDVAKLGEWNNNTAADKQPYEKKAAKLEKYEKIDIAAYRAKGPDAAKKGVVKAEK 180
DB 121 SIGDVAKLGEWNNNTAADKQPYEKKAAKLEKYEKIDIAAYRAKGPDAAKKGVVKAEK 180
QY 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
DB 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 3
US-11-186-422-12
; Sequence 12, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; PRIOR FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-186-422-12

Query Match      99.4%; Score 1142; DB 7; Length 215;
Best Local Similarity 99.1%; Pred. No. 8.8e-77;
Matches 213; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKGDPPKPRGMSSVAFFVQTCREHHKKHPDASVNFSEFSKCCSERWKTMSAKEKGKF 60
DB 1 MGKGDPPKPRGMSSVAFFVQTCREHHKKHPDASVNFSEFSKCCSERWKTMSAKEKGKF 60
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKPKDPNAPRPPSAFFLFCSEYRPKIKGHPGL 120
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKPKDPNAPRPPSAFFLFCSEYRPKIKGHPGL 120
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DB 61 EDMAKADKARYEREMKTYIPPKGETKKKPKDPNAPRPPSAFFLFCSEYRPKIKGHPGL 120
QY 121 SIGDVAKLGEWNNNTAADKQPYEKKAAKLEKYEKIDIAAYRAKGPDAAKKGVVKAEK 180
DB 121 SIGDVAKLGEWNNNTAADKQPYEKKAAKLEKYEKIDIAAYRAKGPDAAKKGVVKAEK 180
QY 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
DB 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 4
US-11-169-041-192
; Sequence 192, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 192
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-192

Query Match      71.8%; Score 824.5; DB 7; Length 879;
Best Local Similarity 85.4%; Pred. No. 6e-53;
Matches 158; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

QY 20 VQTCREHHKKHPDASVNFSEFSKCCSERWKTMSAKEKGKPEDMAKADKARYEREMKTYI 79
DB 695 VDPC-EEHKKKPNPDASVPFSEFLKKCSETWKTITFAKEKGFEDMAKADKARYEREMKTYI 753
QY 80 PPKGETKKKFKDPNAPRPPSAFFLFCSEYRPKIKGHPGLSIGDVAKLGEWNNNTAAD 139
DB 754 PPKGEKKKKFKDPNAPRPPPLAFFLFCSEYRPKIKGHPGLSIDDVVKLAGWNNNTAA 813
QY 140 DQPYEKKAAKLEKYEKIDIAAYRAKGPDAAKKGVVKAEKSKKKKEEEDDEDEDEDE 199
DB 814 DQPYEKKAAKLEKYEKIDIAAYRAKGPNSAKGRVVVKAEKSKKKKEEEDDEDEDEDE 873
QY 200 EDEE 204
DB 874 EEDDD 878

RESULT 5
US-10-821-234-1234
; Sequence 1234, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1234
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; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(169)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1234

Query Match      59.3%; Score 681; DB 6; Length 169;
Best Local Similarity 75.1%; Pred. No. 3.2e-43;
Matches 127; Conservative 13; Mismatches 29; Indels 0; Gaps 0;

Qy 14 SSVAFFVOTCREHHKKHPPDASVNFSEFSKCSRWKTMSSAKGKGFEDMAKADKARYER 73
Db 1 SSVAFFVOTCREHHKKHPPDSSVNFSEFSKCSRWKTMSSAKGKGFEDMAKADKARYDR 60

Qy 74 EMKTYIPPKGETKKFKDPNAPKRPSPAFFLFCSEYRPKIKGHPGLSIGDVAKLGEWM 133
Db 61 EMKNYVPPKGGKGGKDPNAPKRPSPAFFLFCSEHPRKIKSEHPGLSIGDTAKLDEWM 120

Qy 134 NNTAADKQPYEKKAAKLKEKYEKDIAAYRAKGPDAAKGVVKAEEKS 182
Db 121 SEQSGQDKQPYEQEAAVAKEYGKDFAPILPKGKXARKEGSGSPTSSK 169

RESULT 6
US-11-186-422-14
; Sequence 14, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-14

Query Match      32.2%; Score 370; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 6.4e-21;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 NAKRPPSAFFLCSEYRPKIKGHPGLSIGDVAKLGEWMNTAADDKQPYEKKAAKLK 152
Db 1 NAKRPPSAFFLCSEYRPKIKGHPGLSIGDVAKLGEWMNTAADDKQPYEKKAAKLK 60

Qy 153 EYKEDIAA 161
Db 61 EYKEDIAA 69

RESULT 7
US-10-719-150-6
; Sequence 6, Application US/10719150
; Publication No. US20040120953A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Haichao Wang
; TITLE OF INVENTION: ANTAGONISTS OF HMGI FOR TREATING
; TITLE OF INVENTION: INFLAMMATORY CONDITIONS
; FILE REFERENCE: 3268.1000-011
; CURRENT APPLICATION NUMBER: US/10/719,150
```

```
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/10/300,068
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 10/210,747
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 09/503,632
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 09/248,574
; PRIOR FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-719-150-6

Query Match      25.0%; Score 287; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.7e-15;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 PDASVNFSEFSKCSRWKTMSSAKGKGFEDMAKADKARYEREMKTYIPPKGET 85
Db 1 PDASVNFSEFSKCSRWKTMSSAKGKGFEDMAKADKARYEREMKTYIPPKGET 54

RESULT 8
US-11-186-422-13
; Sequence 13, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-13

Query Match      25.0%; Score 287; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.7e-15;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 PDASVNFSEFSKCSRWKTMSSAKGKGFEDMAKADKARYEREMKTYIPPKGET 85
Db 1 PDASVNFSEFSKCSRWKTMSSAKGKGFEDMAKADKARYEREMKTYIPPKGET 54

RESULT 9
US-11-087-099-8879
; Sequence 8879, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8879
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Daucus carota
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Qy 180 KSKKKKEEEDEDEDEDEDEDEDEDE 206
    :| | | :| | :| | :| | :
Db 116 ESDKSKSEVHDDDDDDDDGSEEEEDD 142

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Search completed: April 6, 2006, 10:33:30  
Job time : 26.875 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:33:08 ; Search time 189 Seconds  
(without alignments)  
499.822 Million cell updates/sec

Title: US-10-717-984-1

Perfect score: 215

Sequence: 1 MGKDPKPKMKSSYAFFV.....DESEEDDEDEEDDDDE 215

Scoring table: OLIGO  
Gap 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2442881

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	215	100.0	215	6 ABU07499	Abu07499 Protein d
2	215	100.0	215	6 AAE35859	Aae35859 Human HMG
3	215	100.0	215	7 ADD40789	Add40789 Human HMG
4	215	100.0	215	7 ADD40788	Add40788 Human HMG
5	215	100.0	215	7 ABM85677	Abm85677 Human pro
6	215	100.0	215	8 ADO60491	Ado60491 Human hig
7	215	100.0	215	8 ADO25918	Ado25918 Human hig
8	215	100.0	215	8 ADO71477	Ado71477 Human hig
9	215	100.0	215	8 ADR45922	Adr45922 Human hig
10	215	100.0	215	8 ABM81508	Abm81508 Tumour-as
11	215	100.0	215	9 ADW81011	Adw81011 Amphoteri
12	215	100.0	215	9 ADX69343	Adx69343 Human amp
13	215	100.0	215	9 ADY14248	Ady14248 PRO polyp
14	215	100.0	215	9 ADY85326	Ady85326 Human hig
15	215	100.0	215	9 ADY85085	Ady85085 Human HMG
16	215	100.0	215	9 ADZ80804	Adz80804 Amino aci
17	214	99.5	214	7 ADD47645	Add47645 Human pro
18	214	99.5	214	7 ADE60447	Ade60447 Human pro
19	214	99.5	214	7 ADE57980	Ade57980 Human pro
20	214	99.5	214	7 ADE57984	Ade57984 Human pro
21	214	99.5	214	7 ADE60732	Ade60732 Human pro
22	214	99.5	214	7 ADE60728	Ade60728 Human pro
23	214	99.5	214	8 ADS17580	Adsl7580 Amino aci
24	214	99.5	221	9 ADY85051	Ady85051 Human HMG

## ALIGNMENTS

### RESULT 1

ABU07499  
ID ABU07499 standard; protein; 215 AA.

XX AC ABU07499;

XX DT 28-JAN-2003 (first entry)

XX DB Protein differentially regulated in prostate cancer #102.

XX KW Prostate cancer; gene expression; differential regulation;  
KW molecular marker; drug target; cancer detection; cancer diagnosis;  
KW cancer staging; cancer grading; cancer assessing; cancer monitoring.

XX OS Homo sapiens.

XX PN W0200281638-A2.

XX PD 17-OCT-2002.

XX PF 08-APR-2002; 2002WO-US010824.

XX PR 06-APR-2001; 2001US-0281731P.

XX PR 06-APR-2001; 2001US-0281732P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

PI Sun Z, Jay G;

XX WPI; 2003-058520/05.

DR N-PSDB; ABX10404.

XX Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 413-414; 416pp; English.

CC The invention describes genes (I) which are differentially regulated in prostate cancer. (I) is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer.

CC Preferably, the expression levels of at least 10 genes are determined.  
CC (1) is also useful for identifying agents that modulate a biological  
CC activity of a polypeptide differentially-regulated in prostate cancer  
CC cells, which involves contacting a polypeptide differentially-regulated  
CC in prostate cancer cells with a test agent under conditions effective for  
CC the test agent to modulate a biological activity of the polypeptide, and  
CC determining whether the test agent modulates the biological activity. (1)  
CC is useful as molecular markers, as drug targets, and for detecting,  
CC diagnosing, staging, grading, assessing, monitoring, prognosticating,  
CC preventing or treating, determining predisposition to diseases and  
CC conditions especially relating to prostate cancer. (1) and its expression  
CC products are used in the diagnostic test to assay for presence of cancer  
CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in  
CC blood etc. (1) is useful for assessing cancer e.g., to determine the type  
CC of cancer, its stage of development, the nature of genetic defect, etc.  
CC The polypeptide encoded by (1) can be used as target for therapy or drug  
CC discovery. (1) can also be used for expressing the polypeptide and thus  
CC for searching specific binding partners of the polypeptide. (1) is useful  
CC in therapeutic applications to treat prostate cancer. The identification  
CC of specific genes, and groups of genes, expressed in pathways  
CC physiologically relevant to prostate cancer permits the definition of  
CC functional and disease pathways and the delineation of targets in these  
CC pathways which are useful in diagnostic, therapeutic, and clinical  
CC applications. This is the amino acid sequence of a protein differentially  
CC regulated in prostate cancer  
XX  
SQ Sequence 215 AA;

Query Match 100.0%; Score 215; DB 6; Length 215;  
Best Local Similarity 100.0%; Pred. No. 8.2e-195;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKGDPPKPRGKMSYAFFVQTCREHKKHPPDASVNFSEFSKCSRWKTSKAKGKGF 60  
DB 1 MGKGDPPKPRGKMSYAFFVQTCREHKKHPPDASVNFSEFSKCSRWKTSKAKGKGF 60  
QY 61 EDMAKADKARYEREMKTYIPPKGTGKTKKFKDPNAPKPPPSAFLFCSEYRPKIKGEHPGL 120  
DB 61 EDMAKADKARYEREMKTYIPPKGTGKTKKFKDPNAPKPPPSAFLFCSEYRPKIKGEHPGL 120  
QY 121 SIGDVAKKGEMWNTAADDKQPYEKKAAKLEKYEKDIYAAYRAKGPDAKKGWVKAKE 180  
DB 121 SIGDVAKKGEMWNTAADDKQPYEKKAAKLEKYEKDIYAAYRAKGPDAKKGWVKAKE 180  
QY 181 SKKKKEEEDDE 215  
DB 181 SKKKKEEEDDE 215

RESULT 2  
AAE35859 standard; protein; 215 AA.  
XX AAE35859;  
XX  
DT 17-JUN-2003 (first entry)  
XX Human HMGI protein.  
XX Human; high mobility group; HMGI protein; HMGI A box; HMGI B box; asthma;  
KW inflammatory cytokine; endotoxin shock; rheumatoid arthritis; hepatitis;  
KW appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis;  
KW allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis;  
KW emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis;  
KW Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes;  
KW Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease;  
KW aneobiasis; multiple sclerosis; gout; cerebral infarction; peritonitis;  
KW gene therapy; human immunodeficiency virus; HMGB1 protein.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Binding-site 9. .85  
FT

FT Binding-site /note= "DNA binding motif (HMGI A box)"  
FT 89. .162  
XX /note= "DNA binding motif (HMGI B box)"  
XX  
PN WO200292004-A2.  
XX 21-NOV-2002.  
XX 15-MAY-2002; 2002WO-US015329.  
XX 15-MAY-2001; 2001US-0291034P.  
XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
XX (GEHO) GEN HOSPITAL CORP.  
XX (UYPI-) UNIV PITTSBURGH.  
XX Tracey KJ, Yang H, Warren HS, Fink MP;  
XX WPI; 2003-120594/11.  
XX  
XX New isolated polypeptide having a vertebrate HMGI A box, useful for  
XX inhibiting a condition associated with an activated inflammatory cytokine  
XX cascade, e.g. endotoxin shock, myocardial infarction, asthma, HIV  
XX infection, malaria and diabetes.  
XX Disclosure; Fig 12A; 82pp; English.  
XX  
XX The invention relates to high mobility group (HMG) protein comprising DNA  
XX binding motifs termed HMGI A box and HMGI B box. HMGI A box or a non-  
XX naturally occurring HMGI A box inhibits the release of a pro-inflammatory  
XX cytokine from a vertebrate cell. The methods and compositions of the  
XX invention are useful for inhibiting a condition characterised by  
XX activation of an inflammatory cytokine cascade such as endotoxin shock,  
XX rheumatoid arthritis, appendicitis, peptic or duodenal ulcer, Crohn's  
XX disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,  
XX sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,  
XX filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,  
XX myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout,  
XX cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host  
XX disease, diabetes and Hodgkin's disease. The invention is useful in gene  
XX therapy. The present sequence is human HMGI (also termed as HMGB1)  
XX protein  
XX  
SQ Sequence 215 AA;  
Query Match 100.0%; Score 215; DB 6; Length 215;  
Best Local Similarity 100.0%; Pred. No. 8.2e-195;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKGDPPKPRGKMSYAFFVQTCREHKKHPPDASVNFSEFSKCSRWKTSKAKGKGF 60  
DB 1 MGKGDPPKPRGKMSYAFFVQTCREHKKHPPDASVNFSEFSKCSRWKTSKAKGKGF 60  
QY 61 EDMAKADKARYEREMKTYIPPKGTGKTKKFKDPNAPKPPPSAFLFCSEYRPKIKGEHPGL 120  
DB 61 EDMAKADKARYEREMKTYIPPKGTGKTKKFKDPNAPKPPPSAFLFCSEYRPKIKGEHPGL 120  
QY 121 SIGDVAKKGEMWNTAADDKQPYEKKAAKLEKYEKDIYAAYRAKGPDAKKGWVKAKE 180  
DB 121 SIGDVAKKGEMWNTAADDKQPYEKKAAKLEKYEKDIYAAYRAKGPDAKKGWVKAKE 180  
QY 181 SKKKKEEEDDE 215  
DB 181 SKKKKEEEDDE 215  
RESULT 3  
ADD40789  
ID ADD40789 standard; protein; 215 AA.  
XX  
XX ADD40789;  
AC  
XX  
DT 15-JAN-2004 (first entry)  
XX



XX DE Human HMGB1 protein #2.  
XX KW high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease;  
XX KW contraceptive; endometrium; pregnancy; menstrual cycle irregularity;  
XX KW RAGE; receptor for advanced glycation end; gynaecological; cytostatic;  
XX KW nuclear transcription factor complex; tumour metastasis; endometriosis;  
XX KW polyps; hyperplasia; carcinoma.  
XX OS Homo sapiens.  
XX PN WO2003051383-A2.  
XX PD 26-JUN-2003.  
XX PF 19-DEC-2002; 2002WO-EP014579.  
XX PR 19-DEC-2001; 2001DE-01062556.  
XX PA (ALCE-) ALCEDO BIOTECH GMBH.  
XX PI Bullerdiel J;  
XX DR WPI; 2003-505462/47.  
XX PT Developing treatment and diagnosis of endometrial disorders, using high  
XX PT mobility group B proteins, or related nucleic acid or interaction  
XX PT partners, as targets.  
XX PS Disclosure; SEQ ID NO 3; 43pp; German.  
XX CC This invention describes a novel method comprising using high mobility  
XX CC group B proteins (HMGB) as target molecules for development or  
XX CC preparation of compositions (for treatment, prevention or diagnosis of  
XX CC endometrial diseases, or as contraceptives). The products of the invention  
XX CC are used in kit for characterising the status of the endometrium,  
XX CC especially for presence of pregnancy or irregularities in the menstrual  
XX CC cycle. The proteins used in the invention can be HMGB1, 2 or 3, or SPI00-  
XX CC HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor  
XX CC for advanced glycation end products). The products of the invention have  
XX CC a nuclear transcription factor complex and, extracellularly, a ligand for  
XX CC the surface RAGE (receptor for advanced glycation end products) which is  
XX CC involved in tumour metastasis. The products of the invention are used to  
XX CC develop treatments, preventions or diagnoses of endometrial disease,  
XX CC particularly endometriosis or polyps, hyperplasia or carcinoma of the  
XX CC endometrium, also contraceptives and methods for assessing status of the  
XX CC endometrium, particularly for detecting pregnancy or menstrual disorders.  
XX CC This sequence represents the human HMGB1 protein used in the method of  
XX CC the invention.  
XX SQ Sequence 215 AA;  
Query Match 100.0%; Score 215; DB 7; Length 215;  
Best Local Similarity 100.0%; Pred. No. 8.2e-195;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKGDPPKPKGKSSYAFFVQTCTREEHKKHPDASVNFSEFSKCSRWKTSKEKGKF 60  
DB 1 MGKGDPPKPKGKSSYAFFVQTCTREEHKKHPDASVNFSEFSKCSRWKTSKEKGKF 60  
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKPPSAFFLFCSEYRPKIGEHPL 120  
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKPPSAFFLFCSEYRPKIGEHPL 120  
QY 121 SIGDVAKKLGEMNNTAADKQPEYKKAALKKEKYEKDIAYYRAKGPDAKKGVTAEK 180  
DB 121 SIGDVAKKLGEMNNTAADKQPEYKKAALKKEKYEKDIAYYRAKGPDAKKGVTAEK 180  
QY 181 SKKKKEEEDDE 215  
DB 181 SKKKKEEEDDE 215

RESULT 4  
ADD40788  
ID ADD40788 standard; protein; 215 AA.  
XX AC ADD40788;  
XX DT 15-JAN-2004 (first entry)  
XX DE Human HMGB1 protein.  
XX KW high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease;  
XX KW contraceptive; endometrium; pregnancy; menstrual cycle irregularity;  
XX KW RAGE; receptor for advanced glycation end; gynaecological; cytostatic;  
XX KW nuclear transcription factor complex; tumour metastasis; endometriosis;  
XX KW polyps; hyperplasia; carcinoma.  
XX OS Homo sapiens.  
XX PN WO2003051383-A2.  
XX PD 26-JUN-2003.  
XX PF 19-DEC-2002; 2002WO-EP014579.  
XX PR 19-DEC-2001; 2001DE-01062556.  
XX PA (ALCE-) ALCEDO BIOTECH GMBH.  
XX PI Bullerdiel J;  
XX DR WPI; 2003-505462/47.  
XX DR N-PSDB; ADD40787.  
XX PT Developing treatment and diagnosis of endometrial disorders, using high  
XX PT mobility group B proteins, or related nucleic acid or interaction  
XX PT partners, as targets.  
XX PS Disclosure; Fig 4; 43pp; German.  
XX CC This invention describes a novel method comprising using high mobility  
XX CC group B proteins (HMGB) as target molecules for development or  
XX CC preparation of compositions (for treatment, prevention or diagnosis of  
XX CC endometrial diseases, or as contraceptives). The products of the invention  
XX CC are used in kit for characterising the status of the endometrium,  
XX CC especially for presence of pregnancy or irregularities in the menstrual  
XX CC cycle. The proteins used in the invention can be HMGB1, 2 or 3, or SPI00-  
XX CC HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor  
XX CC for advanced glycation end products). The products of the invention have  
XX CC a gynaecological, contraceptive and cytostatic activity. HMGB is part of a  
XX CC nuclear transcription factor complex and, extracellularly, a ligand for  
XX CC the surface RAGE (receptor for advanced glycation end products) which is  
XX CC involved in tumour metastasis. The products of the invention are used to  
XX CC develop treatments, preventions or diagnoses of endometrial disease,  
XX CC particularly endometriosis or polyps, hyperplasia or carcinoma of the  
XX CC endometrium, also contraceptives and methods for assessing status of the  
XX CC endometrium, particularly for detecting pregnancy or menstrual disorders.  
XX CC This sequence represents the human HMGB1 protein used in the method of  
XX CC the invention.  
XX SQ Sequence 215 AA;  
Query Match 100.0%; Score 215; DB 7; Length 215;  
Best Local Similarity 100.0%; Pred. No. 8.2e-195;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKGDPPKPKGKSSYAFFVQTCTREEHKKHPDASVNFSEFSKCSRWKTSKEKGKF 60  
DB 1 MGKGDPPKPKGKSSYAFFVQTCTREEHKKHPDASVNFSEFSKCSRWKTSKEKGKF 60  
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKPPSAFFLFCSEYRPKIGEHPL 120  
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKPPSAFFLFCSEYRPKIGEHPL 120







PR prostate cancer or tumor.  
PS Claim 12; SEQ ID NO 3888; 7273pp; English.  
XX  
CC The invention relates to human tumour-associated antigenic target (TAT)  
CC polypeptides, and their related nucleic acids. The TAT polypeptides are  
CC overexpressed in cancer tissues compared to normal tissues, and may thus  
CC serve as effective targets for the diagnosis and treatment of cancer in  
CC mammals. The invention also relates to nucleic acid and polypeptide  
CC sequences at least 80% identical to the TAT nucleic acids and  
CC polypeptides; expression vectors and host cells comprising a TAT nucleic  
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic  
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a  
CC TAT polypeptide; and methods and compositions for the treatment or  
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
CC antibodies, antagonists, binding molecules and compositions are useful  
CC for diagnosing or treating a cell proliferative disorder associated with  
CC increased TAT expression, particularly cancers such as breast cancer,  
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
CC used as hybridisation probes, in chromosome and gene mapping, in  
CC chromosome identification and in gene therapy. The present sequence  
CC represents a TAT polypeptide of the invention  
XX  
SQ Sequence 215 AA;  
Query Match 100.0%; Score 215; DB 8; Length 215;  
Best Local Similarity 100.0%; Pred. No. 8.2e-195;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKGDPPKPRGKMSYAFFVQTCTREEHKKHPPDASVNFSEFSKCSRWMTMSAKEGKF 60  
DB 1 MGKGDPPKPRGKMSYAFFVQTCTREEHKKHPPDASVNFSEFSKCSRWMTMSAKEGKF 60  
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPRPPSAFFLCSEYRPKIKGHPGL 120  
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPRPPSAFFLCSEYRPKIKGHPGL 120  
QY 121 SIGDVAKKLGEWNNNTAADDKQYKKAALKKEKYEKIDIAARYAKGKPDAAKGGVWKAKE 180  
DB 121 SIGDVAKKLGEWNNNTAADDKQYKKAALKKEKYEKIDIAARYAKGKPDAAKGGVWKAKE 180  
QY 181 SKKKKEEEDDE 215  
DB 181 SKKKKEEEDDE 215  
RESULT 11  
ADW81011  
XX ADW81011 standard; protein; 215 AA.  
XX AC ADW81011;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Amphoterin protein sequence.  
XX  
KW Vascular endothelial growth factor; VEGF;  
KW vascular endothelial growth factor receptor; VEGFR; dermatological;  
KW edema; gene therapy; vulnerrary; injury; burn; skin cancer; cycostatic;  
KW wound healing; hematoma; pain; necrosis; ischemia; vasotropic;  
KW angiogenesis stimulation; vascularization; tissue regeneration;  
KW amphoterin.  
XX  
OS Homo sapiens.  
XX  
PN WO2005011722-A2.  
XX  
PD 10-FEB-2005.  
XX  
PF 14-JUN-2004; 2004WO-US019197.  
XX

PR 12-JUN-2003; 2003US-0478114P.  
XX 12-JUN-2003; 2003US-0478390P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Saarisalo A, Karkkainen M, Tammela T, Asko-Seljavaara S;  
PI Yla-Herttuala S, He Y;  
XX  
DR WPI; 2005-142834/15.  
XX  
XX Improving healing of skin graft or skin flap to underlying tissue useful  
XX in mastopexy, cosmetic surgery, abdominoplasty, involves using  
XX composition of vascular endothelial growth factor-C or D polynucleotides  
XX and/or polypeptides.  
XX  
XX Example 11; SEQ ID NO 22; 119pp; English.  
XX  
XX The present invention relates to new vascular endothelial growth factor  
XX (VEGF) proteins useful for skin healing of a skin graft onto underlying  
XX tissue. The method involves contacting a skin graft/flap or underlying  
XX tissue with an agent chosen from vascular endothelial growth factor C  
XX (VEGF-C) polynucleotides, VEGF-C polypeptides, VEGF-D polynucleotides,  
XX and VEGF-D polypeptides, in amount effective to reduce edema or increase  
XX perfusion at skin graft or flap. The composition comprises a gene therapy  
XX vector that encodes VEGF-C polynucleotide. The VEGF-C polypeptide  
XX comprises the formula X-B-Z or Z-B-X, where X binds VEGF receptor-3  
XX (VEGFR-3) and comprises a VEGFR-3 ligand amino acid sequence chosen from  
XX a prepro-VEGF-C sequence, and fragments that binds VEGFR-3, where Z  
XX comprises a heparin-binding amino acid sequence, and B comprises a  
XX covalent attachment linking X to Z. The VEGF-C polynucleotides, VEGF-C  
XX polypeptides, VEGF-D polynucleotides, and VEGF-D polypeptides comprise a  
XX VEGF homology domain (VHD) and a heparin-binding domain. Vulnerrary. Gene  
XX therapy. The method is useful in treating skin injury such as burns or  
XX skin cancer, skin grafts, cosmetic surgery, a liposuction procedure, or  
XX in reconstructive surgery. The reconstructive surgery is breast  
XX reconstruction following mastectomy or injury. The subject is diabetic.  
XX The method is useful for improving post-surgical wound healing after  
XX reconstructive and cosmetic surgery and improves complications resulting  
XX from surgery which includes excessive bleeding, such as hematomas,  
XX bruising and wound-healing difficulties, pain, edema, necrosis and  
XX ischemia. The present sequence is amphoterin protein, which contains a  
XX heparin binding domain related to the invention.  
XX  
SQ Sequence 215 AA;  
Query Match 100.0%; Score 215; DB 9; Length 215;  
Best Local Similarity 100.0%; Pred. No. 8.2e-195;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKGDPPKPRGKMSYAFFVQTCTREEHKKHPPDASVNFSEFSKCSRWMTMSAKEGKF 60  
DB 1 MGKGDPPKPRGKMSYAFFVQTCTREEHKKHPPDASVNFSEFSKCSRWMTMSAKEGKF 60  
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPRPPSAFFLCSEYRPKIKGHPGL 120  
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKFPDNPAPRPPSAFFLCSEYRPKIKGHPGL 120  
QY 121 SIGDVAKKLGEWNNNTAADDKQYKKAALKKEKYEKIDIAARYAKGKPDAAKGGVWKAKE 180  
DB 121 SIGDVAKKLGEWNNNTAADDKQYKKAALKKEKYEKIDIAARYAKGKPDAAKGGVWKAKE 180  
QY 181 SKKKKEEEDDE 215  
DB 181 SKKKKEEEDDE 215  
RESULT 12  
ADW69343  
XX ID ADW69343 standard; protein; 215 AA.  
XX  
XX AC ADW69343;  
XX

DT 05-MAY-2005 (first entry)  
XX Human amphoterin.  
XX amphoterin; Heparin binding protein; Neuroprotective; Nootropic;  
XX Antiparkinsonian; Anticonvulsant; VEGF-3 receptor;  
KW Angiogenesis stimulator; Gene Therapy;  
KW vascular endothelial growth factor receptor 3; VEGFR-3;  
KW angiogenesis disorder; neurodegenerative disorder; Alzheimers disease;  
KW Parkinsons disease; motor neurone disease; dementia; paralysis; VEGF-C;  
KW neurological disease; Huntingtons chorea;  
KW vascular endothelial growth factor receptor 3; neurological disease.  
XX Homo sapiens.  
XX WO2005016963-A2.  
XX 24-FEB-2005.  
XX 14-JUN-2004; 2004WO-US019122.  
XX 12-JUN-2003; 2003US-0478114P.  
XX 12-JUN-2003; 2003US-0478390P.  
XX 23-SEP-2003; 2003US-00669176.  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX (LICN ) LICENTIA LTD.  
XX Alitalo K, He Y, Tammela T;  
XX WPI; 2005-182331/19.  
XX New heparin-binding Vascular Endothelial Growth Factor Receptor 3 ligands  
XX comprising prepro-VEGF-C, prepro-VEGF-D sequences or fragments, for  
XX treating neurodegenerative disorder, e.g. Alzheimer's, Parkinson's, or  
XX Huntington's disease.  
XX Disclosure; SEQ ID NO 63; 219pp; English.  
XX The invention relates to heparin-binding vascular endothelial growth  
XX factor receptor 3 (VEGFR-3) proteins and encoding polynucleotides. The  
XX heparin binding VEGFR-3 proteins are used for stimulating  
XX lymphangiogenesis or angiogenesis in a mammal, and for modulating the  
XX growth of mammalian endothelial cells, mammalian endothelial precursor  
XX cells or hematopoietic progenitor cells. The polypeptide may also be used  
XX for promoting recruitment, proliferation, differentiation, migration or  
XX survival of neuronal cells or neuronal precursor cells, and for treating  
XX neurodegenerative disorder, e.g. Alzheimer's disease, Parkinson's  
XX disease, Huntington's disease, motor neuron disease, Amyotrophic Lateral  
XX Sclerosis (ALS), dementia, or cerebral palsy. The present sequence  
XX represents human amphoterin.  
XX Sequence 215 AA;  
Query Match 100.0%; Score 215; DB 9; Length 215;  
Best Local Similarity 100.0%; Pred. No. 8.2e-195;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGKGDPPKPRGKMSYAFFVQTCTREHKKKHDPDASVNFSEFSKKCSERWMTMSAKGKGF 60  
Db 1 MGKGDPPKPRGKMSYAFFVQTCTREHKKKHDPDASVNFSEFSKKCSERWMTMSAKGKGF 60  
Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120  
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120  
Qy 121 SIGDVAKKLGEMWNTAAADKQPYEKKAAKLKEKYEKDAAYRAKGPDAAKKGVVKAKEK 180  
Db 121 SIGDVAKKLGEMWNTAAADKQPYEKKAAKLKEKYEKDAAYRAKGPDAAKKGVVKAKEK 180  
Qy 181 SKKKKEEEDDE 215  
Db 181 SKKKKEEEDDE 215

RESULT 13  
ADY14248  
ID ADY14248 standard; protein; 215 AA.  
XX ADY14248;  
AC AC  
XX 05-MAY-2005 (first entry)  
DT PRO polypeptide SEQ ID NO 54.  
XX  
XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;  
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;  
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;  
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;  
KW Antiallergic; db; gene; diagnosis.  
XX Homo sapiens.  
XX WO2005016962-A2.  
XX 24-FEB-2005.  
XX 11-AUG-2004; 2004WO-US026249.  
XX 11-AUG-2003; 2003US-0493546P.  
XX (GETH ) GENENTECH INC.  
XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;  
XX WPI; 2005-182330/19.  
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and  
XX treating an immune related disorder, e.g. systemic lupus erythematosus,  
XX rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.  
XX Claim 8; SEQ ID NO 54; 158pp; English.  
XX The invention relates to an isolated nucleic acid encoding a PRO  
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,  
XX composition, and method are useful for diagnosing and treating an immune  
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid  
XX arthritis. The present sequence represents a DNA encoding a PRO  
XX polypeptide.  
XX Sequence 215 AA;  
Query Match 100.0%; Score 215; DB 9; Length 215;  
Best Local Similarity 100.0%; Pred. No. 8.2e-195;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGKGDPPKPRGKMSYAFFVQTCTREHKKKHDPDASVNFSEFSKKCSERWMTMSAKGKGF 60  
Db 1 MGKGDPPKPRGKMSYAFFVQTCTREHKKKHDPDASVNFSEFSKKCSERWMTMSAKGKGF 60  
Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120  
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKPPSAFFLFCSEYRPKIKGHPGL 120  
Qy 121 SIGDVAKKLGEMWNTAAADKQPYEKKAAKLKEKYEKDAAYRAKGPDAAKKGVVKAKEK 180  
Db 121 SIGDVAKKLGEMWNTAAADKQPYEKKAAKLKEKYEKDAAYRAKGPDAAKKGVVKAKEK 180  
Qy 181 SKKKKEEEDDE 215  
Db 181 SKKKKEEEDDE 215

RESULT 14  
ADY85326  
ID ADY85326 standard; protein; 215 AA.

AC ADY85326;  
XX 02-JUN-2005 (first entry)  
XX Human high mobility group box protein HMGB1.  
XX High mobility group box; HMGB1; immune disorder; infection;  
XX immunosuppressive; autoimmune disease; allergy; antiasthmatic;  
XX ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.;  
XX Crohn's disease; inflammation; asthma; antiasthmatic;  
XX rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis;  
XX antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX Region 32..85  
XX /label= A\_box  
XX Region 93..161  
XX /label= B\_box  
XX WO2005025604-A2.  
XX 24-MAR-2005.  
XX 10-SEP-2004; 2004WO-US029540.  
XX 10-SEP-2003; 2003US-0502349P.  
XX (GEHO ) GEN HOSPITAL CORP.  
XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
XX Warren HS, Tracey KJ;  
XX WPI; 2005-233421/24.  
XX Treating an immune pathology in an individual comprises administering an  
XX amount of a high mobility group box (HMGB) polypeptide comprising a  
XX vertebrate or a non-naturally occurring HMGB A or B box, or its  
XX immunosuppressive fragment.  
XX Claim 6; SEQ ID NO 1; 57pp; English.  
XX The invention is based on the discovery that high mobility group box  
XX protein 1 (HMGB1, also known as high mobility group-1 or HMGI), when  
XX administered with an antigen, diminishes the antibody response to the  
XX administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B  
XX boxes. A claimed method of treating an immune pathology in an individual  
XX comprises administering a HMGB polypeptide comprising a vertebrate HMGB A  
XX box, a non-naturally-occurring HMGB A box, or an immunosuppressive  
XX fragment of the vertebrate or non-natural HMGB A box. The immune  
XX pathology is induced by the administration of a non-human antigen, non-  
XX self material (e.g. a cell or tissue such as bone marrow cells) or  
XX adjuvant to the individual, by the transplantation of an organ into the  
XX individual, or by infection from a microorganism. Claimed methods of  
XX protecting a subject against an immune pathology, inhibiting an immune  
XX pathology in an individual or decreasing an immune response to an  
XX administered non-human antigen comprise administering a HMGB polypeptide  
XX comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box,  
XX or an immunosuppressive fragment of the vertebrate or non-natural A box.  
XX A claimed method of treating an autoimmune disorder in an individual  
XX comprises administering a HMGB polypeptide comprising a vertebrate HMGB A  
XX box, a non-naturally-occurring HMGB A box, or an immunosuppressive  
XX fragment of these, and a vertebrate or non-naturally-occurring HMGB B  
XX box. The HMGB polypeptide is preferably a HMGB1 peptide and may be  
XX truncated at the C-terminus. The autoimmune disease is allergy,  
XX ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis,  
XX psoriasis or systemic lupus erythematosus (all claimed). The present  
XX sequence is that of the human HMGB1 protein, which can be used as the  
XX HMGB polypeptide in methods of the invention.  
XX Sequence 215 AA;  
XX

Query Match 100.0%; Score 215; DB 9; Length 215;  
Best Local Similarity 100.0%; Pred. No. 8.2e-195;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKGDPKPRGKMSYAFFVQTCREHHKKHPPDASVNFSEFSKCSERWTKMSAKKGF 60  
DB 1 MGKGDPKPRGKMSYAFFVQTCREHHKKHPPDASVNFSEFSKCSERWTKMSAKKGF 60  
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPRPPSAFFLFCSEYRPKIKGEHPGL 120  
DB 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPRPPSAFFLFCSEYRPKIKGEHPGL 120  
QY 121 SIGDAKCLGEMWNTAADDQPYEKAAKLKEKYKDIAAYRAKGPDAKKGVVKAEX 180  
DB 121 SIGDAKCLGEMWNTAADDQPYEKAAKLKEKYKDIAAYRAKGPDAKKGVVKAEX 180  
QY 181 SKKKSEEEDE 215  
DB 181 SKKKSEEEDE 215  
RESULT 15  
ADY85085  
ID ADY85085 standard; protein; 215 AA.  
XX AC ADY85085;  
XX 16-JUN-2005 (first entry)  
XX Human HMGB1 A box.  
XX High mobility group box; HMGB1; monoclonal antibody; antibody therapy;  
XX sepsis; antibacterial immunosuppressive; graft rejection; arthritis;  
XX antiarthritic; asthma; antiasthmatic; lupus erythematosus;  
XX antiinflammatory; inflammation; dermatological;  
XX respiratory distress syndrome; respiratory-gen.; psoriasis;  
XX antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;  
XX peritonitis; burns; vulvovaginitis; ischemia; vasotropic; Behcet's disease;  
XX graft versus host disease; inflammatory bowel disease;  
XX gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;  
XX anabolic; infection; musculoskeletal disease; immune disorder.  
XX Homo sapiens.  
XX Mus sp.  
XX Rattus sp.  
XX WO2005026209-A2.  
XX 24-MAR-2005.  
XX 10-SEP-2004; 2004WO-US029527.  
XX 11-SEP-2003; 2003US-0502568P.  
XX (CRIT-) CRITICAL THERAPEUTICS INC.  
XX Newman W, Qin S, Okeefe T, Obar R;  
XX WPI; 2005-233483/24.  
XX New antibody or its antigen-binding fragment specific to a vertebrate  
XX high mobility group box (HMGB) A box that inhibits release of a  
XX proinflammatory cytokine from a cell treated with HMGB protein, useful  
XX for treating, e.g. sepsis.  
XX Disclosure; SEQ ID NO 2; 123pp; English.  
XX The invention provides antibodies, or their antigen-binding fragments,  
XX that bind to a vertebrate high mobility group box (HMGB) polypeptide, to  
XX methods of detecting and/or identifying an agent that binds to an HMGB  
XX polypeptide, methods of treating a condition in a subject characterized  
XX by activation of an inflammatory cytokine cascade, and methods of



CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-  
CC binding fragment) binds to a vertebrate HMGB A box but does not  
CC specifically bind to non-A box epitopes of HMGB, and inhibits release of  
CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB  
CC protein. A method of treating a condition characterized by activation of  
CC an inflammatory cytokine cascade comprises administering an antibody of  
CC the invention, or its antigen-binding fragment. The condition is selected  
CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult  
CC respiratory distress syndrome, chronic obstructive pulmonary disease,  
CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,  
CC graft versus host disease, inflammatory bowel disease, multiple sclerosis  
CC and cachexia, especially sepsis, arthritis, or lupus. The present  
CC sequence is that of the A box of human HMGB1 ADY85012. An identical  
CC sequence is also found in rat and mouse HMGB1.  
XX  
SQ Sequence 215 AA;

Query Match 100.0%; Score 215; DB 9; Length 215;  
Best Local Similarity 100.0%; Pred. No. 8.2e-195;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGKGDPKKPRGWSSVAFFVQTCREHHKKKHPDASVNFSEFSKCSERWMTMSAKGKF 60  
Db 1 MGKGDPKKPRGWSSVAFFVQTCREHHKKKHPDASVNFSEFSKCSERWMTMSAKGKF 60  
Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFDNAPKRPSPSAFFLFCSEYRPKIKGHPGL 120  
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFDNAPKRPSPSAFFLFCSEYRPKIKGHPGL 120  
Qy 121 SIGDVAKKLGEMWNTAADKQPYEKKAALKKEKYKDIYAAYRAKGPDAAKKGWVKAEK 180  
Db 121 SIGDVAKKLGEMWNTAADKQPYEKKAALKKEKYKDIYAAYRAKGPDAAKKGWVKAEK 180  
Qy 181 SKKKKEEEDDE 215  
Db 181 SKKKKEEEDDE 215

Search completed: April 6, 2006, 10:36:45  
Job time : 189 secs





non-histone chromosomal high-mobility group 1 protein - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I48688; A55402; I57021  
R:Yotov, W.V.; St-Arnaud, R.  
Nucleic Acids Res. 20, 3516, 1992  
A>Title: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mobility group 1 protein (HMG1).  
A:Reference number: I48688; MUID:923335012; PMID:1630928  
A:Accession: I48688  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-215 <RES>  
A:CROSS-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; EMBL:Z11997; NID:G53381; PIDN:AAA20508.1; PI  
R:Ferrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.  
J. Biol. Chem. 269, 28803-28808, 1994  
A>Title: The mouse gene coding for high mobility group 1 protein (HMG1).  
A:Reference number: A55402; MUID:95050689; PMID:7961836  
A:Accession: A55402  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-189, 'E', 191-215 <PER>  
A:CROSS-references: UNIPARC:UPI00000008A6; EMBL:X80457; NID:G620097; PIDN:CAA56631.1; PI  
R:Paiken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.  
Mamm. Genome 5, 91-99, 1994  
A>Title: Molecular cloning, expression analysis, and chromosomal localization of mouse HMG1.  
A:Reference number: I57021; MUID:94235965; PMID:8180479  
A:Accession: I57021  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-215 <RES>  
A:CROSS-references: UNIPARC:UPI00000008A6; EMBL:U00431; NID:G437101; PIDN:AAA20508.1; PI  
C:Genetics:  
A:Gene: hmg1  
A:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C:Keywords: chromosomal protein  
F:6-83/Domain: HMG box homology <HMG1>  
F:92-166/Domain: HMG box homology <HMG2>

Query Match 87.4%; Score 188; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 3.3e-156;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPKPRGKSSYAFFVQTCREHKHKKHPDASVNFSEFSKCSRWKTSKAKGKF 60  
Db 1 MGKGDPKPRGKSSYAFFVQTCREHKHKKHPDASVNFSEFSKCSRWKTSKAKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120  
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120

Qy 121 SIGDVAKKGEMMNNTAADKQPYEKKAAKLKEKYEKIDIAAYRAKGPDAKKGWVKAEK 180  
Db 121 SIGDVAKKGEMMNNTAADKQPYEKKAAKLKEKYEKIDIAAYRAKGPDAKKGWVKAEK 180

Qy 181 SKKKKEE 188  
Db 181 SKKKKEE 188

RESULT 5  
A27853  
nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)  
C:Species: Crictetus griseus (Chinese hamster)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: A27853  
R:Lee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.  
Nucleic Acids Res. 15, 5051-5068, 1987  
A>Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA  
A:Reference number: A27853; MUID:87259986; PMID:3601666  
A:Accession: A27853  
A:Molecule type: mRNA  
A:Residues: 1-170 <LEE>  
A:CROSS-references: UNIPROT:P07156; UNIPARC:UPI000001771D5

C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C:Keywords: chromosomal protein; DNA binding; nucleus  
F:1-38/Domain: HMG box homology (fragment) <HMG1>  
F:47-121/Domain: HMG box homology <HMG2>

Query Match 66.5%; Score 143; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 4.1e-117;  
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 SERKWTSAKEKGFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFL 105  
Db 1 SERKWTSAKEKGFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFL 60

Qy 106 CSEYRPKIKGEHPGLSGDVAKKGEMMNNTAADKQPYEKKAAKLKEKYEKIDIAAYRAK 165  
Db 61 CSEYRPKIKGEHPGLSGDVAKKGEMMNNTAADKQPYEKKAAKLKEKYEKIDIAAYRAK 120

Qy 166 GKPDAAKKGWVKAESKKKKEE 188  
Db 121 GKPDAAKKGWVKAESKKKKEE 143

RESULT 6  
A28897  
nonhistone chromosomal protein HMG-1 - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: A28897  
R:Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.  
Biochemistry 27, 6159-6163, 1988  
A>Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide sequen  
A:Reference number: A28897; MUID:89050965; PMID:3191113  
A:Accession: A28897  
A:Molecule type: mRNA  
A:Residues: 1-215 <TSU>  
A:CROSS-references: UNIPROT:P12682; UNIPARC:UPI000016C6C4; GB:M21684; NID:G16  
C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C:Keywords: chromosomal protein; DNA binding; nucleus  
F:6-83/Domain: HMG box homology <HMG1>  
F:92-166/Domain: HMG box homology <HMG2>

Query Match 65.6%; Score 141; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.7e-115;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPKPRGKSSYAFFVQTCREHKHKKHPDASVNFSEFSKCSRWKTSKAKGKF 60  
Db 1 MGKGDPKPRGKSSYAFFVQTCREHKHKKHPDASVNFSEFSKCSRWKTSKAKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120  
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120

Qy 121 SIGDVAKKGEMMNNTAADK 141  
Db 121 SIGDVAKKGEMMNNTAADK 141

RESULT 7  
S29857  
nonhistone chromosomal protein HMG-1 - human  
C:Species: Homo sapiens (man)  
C>Date: 08-Dec-1993 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S29857  
R:Stros, M.; Dixon, G.H.  
Biochim. Biophys. Acta 1172, 231-235, 1993  
A>Title: A retrospodogene for non-histone chromosomal protein HMG-1.  
A:Reference number: S29857; MUID:93176821; PMID:8439568  
A:Accession: S29857  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-216 <STR>  
A:CROSS-references: UNIPARC:UPI0000011DFAA; EMBL:L08048; NID:G184250; PIDN:AAA64970.1; PI



## RESULT 12

A34719  
nonhistone chromosomal protein HMG-2 - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 06-Jul-1990 #sequence\_revision 06-Jul-1990 #text\_change 09-Jul-2004  
C;Accession: A34719  
R;Shirakawa, H.; Tsuda, K.; Yoshida, M.  
Biochemistry 29, 4419-4423, 1990  
A;Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nucle  
A;Reference number: A34719; MUID:90275208; PMID:2350545  
A;Accession: A34719  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-210 <SHI>  
A;Cross-references: UNIPROT:P17741; UNIPARC:UPI0000166C65; GB:J02895; NID:g164491; PIDN:  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein; DNA binding; nucleus  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 12.1%; Score 26; DB 2; Length 210;  
Best Local Similarity 100.0%; Pred. No. 3.4e-15;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPRGKMSSYAFFVQTCREHKKKHPD 33  
|||||  
Db 8 KPRGKMSSYAFFVQTCREHKKKHPD 33

## RESULT 13

S54774  
high mobility group 2 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S54774; S52211  
R;Zwilling, S.; Koenig, H.; Wirth, T.  
EMBO J. 14, 1198-1208, 1995  
A;Title: High mobility group protein 2 functionally interacts with the POU domains of o  
A;Reference number: S54774; MUID:95237201; PMID:7720710  
A;Accession: S54774  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-210 <ZWI>  
A;Cross-references: UNIPROT:P30681; UNIPARC:UPI000016432C; EMBL:Z46757; NID:g609168; PID  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 12.1%; Score 26; DB 2; Length 210;  
Best Local Similarity 100.0%; Pred. No. 3.4e-15;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPRGKMSSYAFFVQTCREHKKKHPD 33  
|||||  
Db 8 KPRGKMSSYAFFVQTCREHKKKHPD 33

## RESULT 14

S68823  
HMG1 protein homolog, 6K - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 02-Jul-1998  
C;Accession: S68823  
R;Sparatore, B.; Melloni, E.; Patrone, M.; Passalacqua, M.; Pontremoli, S.  
PESS Lett. 385, 95-98, 1996  
A;Title: A 6 kDa protein homologous to the N-terminus of the HMG1 protein promoting stim  
A;Reference number: S68823; MUID:96228042; PMID:8647297  
A;Accession: S68823  
A;Molecule type: mRNA  
A;Residues: 1-54 <SPA>  
A;Cross-references: UNIPARC:UPI00001771DD  
A;Experimental source: C44 MEL cells  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology

F;6-54/Domain: HMG box homology #status atypical <HMG>

Query Match 11.2%; Score 24; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 6.3e-14;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 KKKHPDASVNFSEFSKCKSERWKT 51  
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Db 28 KKKHPDASVNFSEFSKCKSERWKT 51

## RESULT 15

S26062  
nonhistone chromosomal protein HMG-2 - mouse  
N;Alternate names: high mobility group 2 protein  
C;Species: Mus musculus (house mouse)  
C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 09-Jul-2004  
C;Accession: S26062; S25487; I48408  
R;Stolzenburg, F.; Dinkl, E.; Grummt, F.  
Nucleic Acids Res. 20, 4927, 1992  
A;Title: Nucleotide sequence of a mouse cDNA encoding the non-histone chromosomal high m  
A;Reference number: I48408; MUID:93027215; PMID:1408807  
A;Accession: S26062  
A;Molecule type: mRNA  
A;Residues: 1-205 <STO>  
A;Cross-references: UNIPROT:P30681; UNIPARC:UPI000016CDD8; EMBL:X67668; NID:g51338; PIDN:  
A;Note: this is a revision to the sequence from reference S25487  
R;Stolzenburg, F.; Dinkl, E.; Grummt, F.  
submitted to the EMBL Data Library, August 1992  
A;Reference number: S25487  
A;Accession: S25487  
A;Molecule type: mRNA  
A;Residues: 1-183, 'KNDSED', 190-195, 'E', 197-198, 'ED', 201-202, 'G', 204-205, 'EDEE' <STW>  
A;Cross-references: UNIPARC:UPI00001771D1; EMBL:X67668  
A;Note: this sequence has been revised in reference S26062  
C;Genetics:  
A;Gene: hmg2  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein; DNA binding; nucleus  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 10.2%; Score 22; DB 2; Length 205;  
Best Local Similarity 100.0%; Pred. No. 1e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GKMSYAFFVQTCREHKKKHP 32  
|||||  
Db 11 GKMSYAFFVQTCREHKKKHP 32

Search completed: April 6, 2006, 10:41:29  
Job time : 42 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:33:48 ; Search time 231 Seconds  
(without alignment)  
656.661 Million cell updates/sec

Title: US-10-717-984-1

Perfect score: 215

Sequence: 1 MGKGDPKPKGKMSYAFFV.....DEEEDEDEDEDEDDDE 215

Scoring table:

OLIGO  
Gapop 60.0 , Gapext 60.0  
2166443 seqs, 705528306 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	215	100.0	215	2	Q5T7C3_HUMAN
2	215	100.0	215	2	Q4R844_MACFA
3	214	99.5	214	1	HMG1_CANFA
4	214	99.5	214	1	HMG1_HUMAN
5	205	95.3	214	1	HMG1_BOVIN
6	192	89.3	192	2	Q5T7C5_HUMAN
7	189	87.9	215	2	Q9QWY6_SPAEH
8	188	87.4	215	2	Q548R9_RAT
9	188	87.4	215	2	Q58EV5_MOUSE
10	187	87.0	214	1	HMG1_MOUSE
11	187	87.0	214	1	HMG1_RAT
12	181	84.2	181	2	Q8BNM0_MOUSE
13	178	82.8	178	2	Q8C7C4_MOUSE
14	160	74.4	215	2	Q9QX40_SPAEH
15	157	73.0	157	2	Q5T7C2_HUMAN
16	157	73.0	158	2	Q5T7C4_HUMAN
17	157	73.0	176	2	Q59GW1_HUMAN
18	153	71.2	180	1	HMG1_CRIGR
19	146	67.9	162	2	Q5T7C6_HUMAN
20	143	66.5	215	2	Q88611_SPAEH
21	140	65.1	214	1	HMG1_PIG
22	137	63.7	215	2	Q143Z1_HUMAN
23	132	61.4	132	2	Q5T7C1_HUMAN
24	128	59.5	215	2	Q88612_SPAEH
25	99	46.0	215	2	Q6P202_MOUSE
26	97	45.1	97	2	Q5T7C0_HUMAN
27	97	45.1	215	2	Q8BQ02_MOUSE
28	92	42.8	211	1	HMG1X_HUMAN
29	92	42.8	234	2	Q7TPK9_RAT
30	58	27.0	214	2	Q9PUK9_CHICK
31	58	27.0	215	2	Q9YH06_CHICK

```

RESULT 1
Q5T7C3_HUMAN
ID Q5T7C3_HUMAN PRELIMINARY; PRT; 215 AA.
AC Q5T7C3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE High-mobility group box 1.
GN Name=HMG1; ORFNames=RP11-550P23.1-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL353648; CAIL5600.1; -; Genomic_DNA.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;

Query Match 100.0%; Score 215; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-184;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPKPKGKMSYAFFVQTCREHHKXKHPDASVNFSEFSKCSRWKTSKKEGKF 60
Db 1 MGKGDPKPKGKMSYAFFVQTCREHHKXKHPDASVNFSEFSKCSRWKTSKKEGKF 60

Qy 61 EDMAKADKARYEMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120

Qy 121 SIGDVAKKLGEWNNNTAADKQPYEKKAALKKEKYEKDIAAYRAKGPDAKKGWVKAEK 180
Db 121 SIGDVAKKLGEWNNNTAADKQPYEKKAALKKEKYEKDIAAYRAKGPDAKKGWVKAEK 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 2
Q4R844_MACFA
ID Q4R844_MACFA PRELIMINARY; PRT; 215 AA.
AC Q4R844;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Testis cDNA clone: Qc9A-13487, similar to human high-mobility group

```

```

32 54 25.1 206 2 Q5BKQ1_MOUSE Q5bkq1 mus musculu
33 50 23.3 50 2 Q9NYD7_HUMAN Q9nyd7 homo sapien
34 39 18.1 211 2 Q6PAN5_XENTR Q6pan5 xenopus tro
35 39 18.1 211 2 Q7SZ42_XENLA Q7sz42 xenopus lae
36 37 17.2 208 2 Q80YZ1_MOUSE Q80yz1 mus musculu
37 35 16.3 211 2 Q9NQJ4_HUMAN Q9nqj4 homo sapien
38 31 14.4 38 1 HMG2_BOVIN P40673 bos taurus
39 30 14.0 55 2 Q7TPS2_MOUSE Q7tps2 mus musculu
40 30 14.0 205 2 Q6NX86_BRARE Q6nx86 brachydanio
41 30 14.0 205 2 Q7ZVC6_BRARE Q7zvc6 brachydanio
42 29 13.5 204 1 HMG1_ONCMY P07746 oncorhynchu
43 27 12.6 191 2 Q75MM1_HUMAN Q75mm1 homo sapien
44 26 12.1 190 2 Q9CT19_MOUSE Q9ct19 mus musculu
45 26 12.1 195 2 Q96J53_HUMAN Q96j53 homo sapien

```

## ALIGNMENTS

DE box 1 (HMGBl),.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
[1]  
RN NUCLEOTIDE SEQUENCE.  
RP International consortium for macaque cDNA sequencing, analysis;  
RA "DNA sequences of macaque genes expressed in brain or testis and its  
RT evolutionary implications."; to the EMBL/GenBank/DBJ databases.  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP Oseada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,  
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.,  
RT Substitution rate and structural divergence of 5'UTR evolution;  
RT Comparative analysis between human and cynomolgus monkey cDNAs.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB168615; BAB00728.1; -; mRNA.  
SQ SEQUENCE 215 AA; 24894 MW; 8A866CF277D417B5 CRC64;  
  
Query Match 100.0%; Score 215; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.2e-184;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MGKGDPPKPRGKSSYAFFVQTCEEHKKKHPDASVNFSEFSKCSERWMTSAKKGKF 60  
DB 1 MGKGDPPKPRGKSSYAFFVQTCEEHKKKHPDASVNFSEFSKCSERWMTSAKKGKF 60  
  
QY 61 EDMAKADKARYEREMKTYIIPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKGEHPGL 120  
DB 61 EDMAKADKARYEREMKTYIIPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKGEHPGL 120  
  
QY 121 SIGDVAKKLGEMWNNTAADKQPYEKKAAKLKEKYEDIAAYRAKGPDAKKGVVKAKE 180  
DB 121 SIGDVAKKLGEMWNNTAADKQPYEKKAAKLKEKYEDIAAYRAKGPDAKKGVVKAKE 180  
  
QY 181 SKKKKEEEDDE 215  
DB 181 SKKKKEEEDDE 215

RESULT 3  
HMG1\_CANFA  
ID\_HMG1\_CANFA STANDARD; PRT; 214 AA.  
AC Q6YK44;  
DT 10-MAY-2005 (Rel. 47, Created)  
DT 10-MAY-2005 (Rel. 47, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE High mobility group protein 1 (HMG-1) (High mobility group protein  
DE Bl).  
GN Name=HMGBl;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.  
OX NCBI\_TaxID=9615;  
[1]  
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].  
RP MEDLINE=22932580; PubMed=14571134; DOI=10.1159/000073415;  
RA Murua Escobar H., Meyer B., Richter A., Becker K., Flohr A.M.,  
RA Bullerdiek J., Nolte I.;  
RT "Molecular characterization of the canine HMGBl.";  
RL Cytogenet. Genome Res. 101:33-38 (2003).  
CC -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds  
CC double stranded DNA (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.  
CC -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration -  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC

CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; AY135519; AAN11296.1; -; mRNA.  
DR EMBL; AY135521; AAN11319.1; -; Genomic\_DNA.  
DR HSSP; P07155; 1AAB.  
DR SMR; Q6YK44; 1-83, 92-170.  
DR Ensembl; ENSCARG0000006597; Canis familiaris.  
DR InterPro; IPR000135; Highmobility\_12.  
DR Pfam; PF00505; HMG\_12\_box.  
DR PRINTS; PR00886; HIGHMOBLTY12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS00353; HMG\_BOX\_1; 1.  
DR PROSITE; PS01118; HMG\_BOX\_2; 2.  
KW Chromosomal protein; DNA-Binding; Nuclear protein; Repeat.  
FT INIT MET 0 By similarity.  
FT DNA\_BIND 8 78 HMG box 1.  
FT COMBIAS 185 214 Asp/Glu-rich (acidic).  
FT SEQUENCE 214 AA; 24763 MW; B3C6A80FC7F0F433 CRC64;  
  
Query Match 99.5%; Score 214; DB 1; Length 214;  
Best Local Similarity 100.0%; Pred. No. 9.7e-184;  
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 GKGDPPKPRGKSSYAFFVQTCEEHKKKHPDASVNFSEFSKCSERWMTSAKKGKF 61  
DB 1 GKGDPPKPRGKSSYAFFVQTCEEHKKKHPDASVNFSEFSKCSERWMTSAKKGKF 60  
  
QY 62 DMAKADKARYEREMKTYIIPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKGEHPGLS 121  
DB 61 DMAKADKARYEREMKTYIIPKGETKKKFPDNPAPKPPSAFFLFCSEYRPKIKGEHPGLS 120  
  
QY 122 IGDVAKKLGEMWNNTAADKQPYEKKAAKLKEKYEDIAAYRAKGPDAKKGVVKAES 181  
DB 121 IGDVAKKLGEMWNNTAADKQPYEKKAAKLKEKYEDIAAYRAKGPDAKKGVVKAES 180  
  
QY 182 KKKKEEEDDE 215  
DB 181 KKKKEEEDDE 214

RESULT 4  
HMG1\_HUMAN  
ID\_HMG1\_HUMAN STANDARD; PRT; 214 AA.  
AC P09429; Q6TBE1;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE High mobility group protein 1 (HMG-1) (High mobility group protein  
DE Bl).  
GN Name=HMGBl; Synonyms=HMG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN NUCLEOTIDE SEQUENCE [MRNA].  
RP MEDLINE=89160247; PubMed=2922262;  
RA Wen L., Huang J.K., Johnson B.H., Reek G.R.;  
RT "A human placental cDNA clone that encodes nonhistone chromosomal  
RT protein HMG-1.";  
RL Nucleic Acids Res. 17:1197-1214 (1989).  
[2]  
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RP MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;  
RA Ferrari S., Finelli P., Rocchi M., Bianchi M.E.;  
RT "The active gene that encodes human high mobility group 1 protein  
RT (HMG1) contains introns and maps to chromosome 13.";  
RL Genomics 35:367-371 (1996).

[3] NUCLEOTIDE SEQUENCE [MRNA].  
RP He F.T., Yang Z.H., Ji Q., Li R., Peng J., Jiang Y., Zhong X.;  
RA Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
[4]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RP TISSUE=Small intestine;  
RG The German CDNA consortium;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
[5]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RP Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
RA "Cloning of human full open reading frames in Gateway(TM) system entry  
RT vector (pDONR201).";  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
[6]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RP Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RT "Cloning of human full-length cDNAs in BD Creator(TM) system donor  
RT vector";  
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
[7]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RP TISSUE=Brain, Cervix, and Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Sapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[8]  
RN PROTEIN SEQUENCE OF 57-64 AND 112-126.  
RP TISSUE=Mammary carcinoma;  
RX MEDLINE=97295304; PubMed=9150946;  
RA Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,  
RA Simpson R.J., Dorow D.S.;  
RT "Two-dimensional electrophoretic analysis of human breast carcinoma  
RT proteins: mapping of proteins that bind to the SH3 domain of mixed  
RT lineage kinase MLK2.";  
RL Electrophoresis 18:588-598(1997).  
CC -I- FUNCTION: Binds preferentially single-stranded DNA and unwinds  
CC double stranded DNA.  
CC -I- INTERACTION:  
CC P04637:TP53; NBEsp1; InAct=EBI-389432, EBI-366083;  
CC O15350:TP73; NBEsp1; InAct=EBI-389432, EBI-389606;  
CC -I- SUBCELLULAR LOCATION: Nuclear.  
CC -I- SIMILARITY: Belongs to the HMGI/HMG2 protein family.  
CC -I- SIMILARITY: Contains 2 HMG box DNA-binding domains.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; X12597; CAA31110.1; -; mRNA.

DR EMBL; U51677; AAB08987.1; -; Genomic\_DNA.  
DR EMBL; AY377859; AAQ91389.1; -; mRNA.  
DR EMBL; CY749614; CAH18408.1; -; mRNA.  
DR EMBL; CR456863; CAG33144.1; -; mRNA.  
DR EMBL; BT020159; AAF35586.1; -; mRNA.  
DR EMBL; BC003378; AAH33378.1; -; mRNA.  
DR EMBL; BC030381; AAH30381.1; -; mRNA.  
DR EMBL; BC067732; AAH67732.1; -; mRNA.  
DR PIR; S02826; S02826.  
DR HSSP; P07156; INHN.  
DR SMR; P09429; 1-83, 92-170.  
DR IntAct; P09429; -  
DR Ensembl; ENSG00000189403; Homo sapiens.  
DR HGNC; HGNC:4983; HMGB1.  
DR H-InvDB; HIX0011209; -.  
DR MIM; 163905; -.  
DR GO; GO:0000793; C:Condensed chromosome; IDA.  
DR GO; GO:0008301; F:DNA bending activity; TAS.  
DR GO; GO:0008134; F:Transcription factor binding; TAS.  
DR GO; GO:0006288; P:base-excision repair, DNA ligation; IDA.  
DR GO; GO:0006310; P:DNA recombination; TAS.  
DR GO; GO:0006281; P:DNA repair; TAS.  
DR GO; GO:0006268; P:DNA unwinding; NAS.  
DR GO; GO:0006325; P:establishment and/or maintenance of chromatin; TAS.  
DR GO; GO:001055; P:negative regulation of transcriptional preinitiation; IDA.  
DR GO; GO:0006357; P:regulation of transcription from RNA polymerase; IDA.  
DR InterPro; IPR000135; Highmobility 12.  
DR InterPro; IPR000910; HMG 12\_box.  
DR Pfam; PF00505; HMG box; 2.  
DR PRINTS; PR0886; HIGHMOBILITY12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS00353; HMG\_BOX\_1; 1.  
DR PROSITE; PS01118; HMG\_BOX\_2; 2.  
KW Chromosomal protein; Direct protein sequencing; DNA-binding;  
KW Nuclear protein; Repeat.  
FT INIT\_MET 0 0  
FT DNA\_BIND 8 78 HMG box 1.  
FT COMPBIAS 94 162 HMG box 2.  
FT COMPBIAS 185 214 Asp/Glu-rich (acidic).  
FT CONFLICT 214 214 E -> D (in Ref. 5).  
SQ SEQUENCE 214 AA; 24763 MW; B3C6A80FC7F0F433 CRC64;  
Query Match 99.5%; Score 214; DB 1; Length 214;  
Best Local Similarity 100.0%; Pred. No. 9.7e-184;  
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GKGDPPKPRGKMSYAFFVQTCREEHKKHPDASVNFSEFSKCKSERWKTMSAKEKGF 61  
DB 1 GKGDPPKPRGKMSYAFFVQTCREEHKKHPDASVNFSEFSKCKSERWKTMSAKEKGF 60  
QY 62 DMAKADKARYEREMKTYIPPKGTGKTKKFKDPNAPKRPSPAFFLFCSEYRPRKIKGHPGLS 121  
DB 61 DMAKADKARYEREMKTYIPPKGTGKTKKFKDPNAPKRPSPAFFLFCSEYRPRKIKGHPGLS 120  
QY 122 IGVAVKGLGEMWNTAADDKQPYEKKAALKYKEDIAAYRAKGPDAKKGVVAEKS 181  
DB 121 IGVAVKGLGEMWNTAADDKQPYEKKAALKYKEDIAAYRAKGPDAKKGVVAEKS 180  
QY 182 KKKEEEDDE 215  
DB 181 KKKEEEDDE 214  
RESULT 5  
HMGB1\_BOVIN STANDARD; PRT; 214 AA.  
AC P10103;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE High mobility group protein 1 (HMG-1) (High mobility group protein

DE B1).  
GN Name=HMG1; Synonyms=HMG1;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC STRAIN=Holstein; TISSUE=Fetal thymus;  
RX MEDLINE=89057489; PubMed=3194213;  
RA Kaplan D.J., Duncan C.H.;  
RT "Full length cDNA sequence for bovine high mobility group 1 (HMG1)  
RL Nucleic Acids Res. 16:10375-10375(1988).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA] OF 115-214.  
RX MEDLINE=84128872; PubMed=6141822;  
RA Pentecost B., Dixon G.H.;  
RT "Isolation and partial sequence of bovine cDNA clones for the high-  
RL mobility-group protein (HMG-1).";  
RN Biosci. Rep. 4:49-57(1984).  
RN [3]  
RP PROTEIN SEQUENCE OF 1-37; 45-156 AND 158-194.  
RX MEDLINE=81138849; PubMed=7202717; DOI=10.1016/0014-5793(80)80453-4;  
RA Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.;  
RT "The primary structures of non-histone chromosomal proteins HMG 1 and  
RL 2.";  
RN FEBS Lett. 122:264-270(1980).  
RN [4]  
RP PROTEIN SEQUENCE OF 1-36.  
RX MEDLINE=90306387; PubMed=2365081; DOI=10.1016/0014-5793(90)80308-6;  
RA Christen T., Bischoff M., Hobi R., Kuenzle C.C.;  
RT "High mobility group proteins 1 and 2 bind preferentially to  
RL brominated poly(dG-dC).poly(dG-dC) in the Z-DNA conformation but not  
RL to other types of Z-DNA".  
RN FEBS Lett. 267:139-141(1990).  
CC 1- FUNCTION: Binds preferentially single-stranded DNA and unwinds  
CC double stranded DNA.  
CC 1- SUBCELLULAR LOCATION: Nuclear.  
CC 1- SIMILARITY: Belongs to the HMG1/HMG2 protein family.  
CC 1- SIMILARITY: Contains 2 HMG box DNA-binding domains.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; X12796; CAA31284.1; -; mRNA.  
CC EMBL; M26110; AAA30567.1; -; mRNA.  
CC PIR; S01947; S01947.  
CC HSSP; P07156; INHN.  
CC SNR; P10103; 1-83, 92-170.  
CC GO; GO:0000793; C:condensed chromosome; ISS.  
CC GO; GO:0008301; F:DNA bending activity; ISS.  
CC GO; GO:0005515; F:protein binding; ISS.  
CC GO; GO:0006288; F:base-excision repair; DNA ligation; ISS.  
CC GO; GO:0006310; P:base recombination; ISS.  
CC GO; GO:0006281; P:DNA repair; ISS.  
CC GO; GO:0006268; P:DNA unwinding; ISS.  
CC GO; GO:0006325; P:establishment and/or maintenance of chromat. .; ISS.  
CC GO; GO:0017055; P:negative regulation of transcriptional prei. .; ISS.  
CC InterPro; IPR000135; Highmobility\_12.  
CC InterPro; IPR000910; HMG\_12\_box.  
CC Pfam; PF00505; HMG\_box; 2.  
CC PRINTS; PR00886; HIGHMOBILITY12.  
CC SMART; SM00398; HMG; 2.  
CC PROSITE; PS00353; HMG\_BOX\_1; 1.  
CC PROSITE; PS00118; HMG\_BOX\_2; 2.  
KW Chromosomal protein; Direct protein sequencing; DNA-binding;  
KW Nuclear protein; Repeat.  
FT INIT\_MET 0 0

	DNA_BIND	8	78	HMG box 1.
FT	DNA_BIND	94	162	HMG box 2.
FT	COMPBIAS	185	214	Asp/Glu-rich (acidic).
FT	CONFLICT	22	22	C -> S (in Ref. 3).
FT	CONFLICT	105	105	C -> A (in Ref. 3).
FT	CONFLICT	115	119	EHPGL -> PGGGV (in Ref. 2).
FT	CONFLICT	193	193	E -> D (in Ref. 3).
SQ	SEQUENCE	214 AA;	24777 MW;	B283A80FC7F0F433 CRC64;

Query Match 95.3%; Score 205; DB 1; Length 214;  
Best Local Similarity 100.0%; Pred. No. 1.2e-175;  
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	2	GKGDPPKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGKFE	61
Db	1	GKGDPPKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGKFE	60
QY	62	DMAKADKARYEREMKTYIIPKGTGKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGLS	121
Db	61	DMAKADKARYEREMKTYIIPKGTGKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGLS	120
QY	122	IGDVAKKLGEMWNTAADDKQPYEKKAALKKEKYEKDIAAYRAKGPDAKKGWVAEKS	181
Db	121	IGDVAKKLGEMWNTAADDKQPYEKKAALKKEKYEKDIAAYRAKGPDAKKGWVAEKS	180
QY	182	KKKKEEEDDE	206
Db	181	KKKKEEEDDE	205

RESULT 6  
Q5T7C5 HUMAN  
ID Q5T7C5\_HUMAN PRELIMINARY; PRT; 192 AA.  
AC Q5T7C5; 2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE High-mobility group box 1 (fragment).  
GN Name=HMG1; ORFNames=RP11-550P23.1-001;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Pelan S.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL353648; CA115602.1; -; Genomic\_DNA.  
DR SNR; Q5T7C5; 2-84, 93-171.  
DR GO; GO:0000785; C:chromatin; IEA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR000135; Highmobility\_12.  
DR InterPro; IPR000910; HMG\_12\_box.  
DR Pfam; PF00505; HMG\_box; 2.  
DR PRINTS; PR00886; HIGHMOBILITY12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS00353; HMG\_BOX\_1; 1.  
DR PROSITE; PS00118; HMG\_BOX\_2; 2.  
FT NON TER 192 192  
SQ SEQUENCE 192 AA; 22050 MW; 6A52DB61DA307C1D CRC64;

Query Match 89.3%; Score 192; DB 2; Length 192;  
Best Local Similarity 100.0%; Pred. No. 5e-164;  
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKGDPKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGKGF	60
Db	1	MKGDPKPRGKMSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGKGF	60
QY	61	EDNAKADKARYEREMKTYIIPKGTGKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL	120

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Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120
Qy 121 SIGDVAKKLGEMWNTAADKKQPYEKKAALKKEKYEKDIAAYRAKGPDAAKGVVKAEK 180
Db 121 SIGDVAKKLGEMWNTAADKKQPYEKKAALKKEKYEKDIAAYRAKGPDAAKGVVKAEK 180
Qy 181 SKKKKEEEDDE 192
Db 181 SKKKKEEEDDE 192

RESULT 7
Q9QY6 SPAEH PRELIMINARY; PRT; 215 AA.
ID Q9QY6 SPAEH PRELIMINARY; PRT; 215 AA.
AC Q9QY6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE High mobility group protein.
GN Name=HMG1;
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Spalacinae; Nannospalax.
OX NCBI_TaxID=30637;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee K.-L., D., Lum H.-K., Nevo E.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF078819; AAC27652.1; -, Genomic_DNA.
DR HSP; P07156; INHN.
DR SMR; Q9QY6; 2-84, 93-171.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; H1gHmobility_12.
DR InterPro; IPR000910; HMG_box_2.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBLTY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS00118; HMG_BOX_2; 2.
SQ SEQUENCE 215 AA; 24822 MW; D20D659274B575B4 CRC64;

Query Match 87.9%; Score 189; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e-161; Mismatches 0; Indels 0; Gaps 0;
Matches 189; Conservative 0;

Qy 27 HKKKHPDASVNFSEFSKCSERWKTMSAKGKGFEDMAKADKARYEREMKTYIPPKGETK 86
Db 27 HKKKHPDASVNFSEFSKCSERWKTMSAKGKGFEDMAKADKARYEREMKTYIPPKGETK 86
Qy 87 KKFDPNAPKPPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADKKQPYEK 146
Db 87 KKFDPNAPKPPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADKKQPYEK 146
Qy 147 KAAKLEKYEKDIAAYRAKGPDAAKGVVKAESKKKKKEEEDDEDEDEDEDEDEDEDE 206
Db 147 KAAKLEKYEKDIAAYRAKGPDAAKGVVKAESKKKKKEEEDDEDEDEDEDEDEDEDE 206
Qy 207 DEBEDDDDE 215
Db 207 DEBEDDDDE 215

RESULT 8
Q548R9 RAT PRELIMINARY; PRT; 215 AA.
ID Q548R9 RAT PRELIMINARY; PRT; 215 AA.
AC Q548R9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
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DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Amphoterin.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ito T., Suzuki A., Horimoto N., Imai E., Hori M.;
RT "Amphoterin is associated with the development of the kidney.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275734; AAF82799.1; -, mRNA.
SQ SEQUENCE 215 AA; 24894 MW; 8A868DE266552B5 CRC64;

Query Match 87.4%; Score 188; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.2e-160; Mismatches 0; Indels 0; Gaps 0;
Matches 188; Conservative 0;

Qy 1 MGKGDPPKPRGKSSSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGF 60
Db 1 MGKGDPPKPRGKSSSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWKTMSAKEKGF 60
Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120
Qy 121 SIGDVAKKLGEMWNTAADKKQPYEKKAALKKEKYEKDIAAYRAKGPDAAKGVVKAEK 180
Db 121 SIGDVAKKLGEMWNTAADKKQPYEKKAALKKEKYEKDIAAYRAKGPDAAKGVVKAEK 180
Qy 181 SKKKKEE 188
Db 181 SKKKKEE 188

RESULT 9
Q58EV5 MOUSE PRELIMINARY; PRT; 215 AA.
ID Q58EV5 MOUSE PRELIMINARY; PRT; 215 AA.
AC Q58EV5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE High mobility group box 1 (16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130064K11 product:high mobility group box 1, full insert sequence) (13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330050N16 product:high mobility group box 1, full insert sequence).
GN Name=Hmgbl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=FVB/N; TISSUE=Colon, and Mammary tumor. C3;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=FVB/N; TISSUE=Colon;  
RG NIH MGC Project;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bargh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nkaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Clothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Giassi C., Godzik A., Gough J.,  
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RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
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RN [27]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [28]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [29]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [30]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [31]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [32]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [33]  
RP NUCLEOTIDE SEQUENCE.  
RN STRAIN=C57BL/6J; TISSUE=Heart;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.15



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DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBLTY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS01118; HMG_BOX_2; 2.
SQ SEQUENCE 215 AA; 24894 MW; 8A868DE266D552B5 CRC64;

Query Match 87.4%; Score 188; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.2e-160;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKGDPPKPRGMSYAFFVQTCEEHKKHPDASVNFSPSKCSRWKTMSSAKGKGF 60
DB 1 MGKGDPPKPRGMSYAFFVQTCEEHKKHPDASVNFSPSKCSRWKTMSSAKGKGF 60

QY 61 EDMAKADKARYEREMKTYIPPKGTGKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120
DB 61 EDMAKADKARYEREMKTYIPPKGTGKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120

QY 121 SIGDVAKLGEMWNTAADDKQPYEKKAALKKEKYEKDIAAYRAKGPDAKKGVVKAEX 180
DB 121 SIGDVAKLGEMWNTAADDKQPYEKKAALKKEKYEKDIAAYRAKGPDAKKGVVKAEX 180

QY 181 SKKKKEE 188
DB 181 SKKKKEE 188

RESULT 10
HMG1_MOUSE
ID HMG1_MOUSE STANDARD; PRT; 214 AA.
AC P63158; P07155; P27109; P27428;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE High mobility group protein 1 (HMG-1) (High mobility group protein
DE B1).
GN Name=Hmgbl; Synonyms=Hmg-1, Hmg1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C3H/He;
RX MEDLINE=92335012; PubMed=1630928;
RA Yotov W.V., St Arnaud R.;
RT "Nucleotide sequence of a mouse cDNA encoding the nonhistone
RL chromosomal high mobility group protein-1 (HMG1).";
RL Nucleic Acids Res. 20:3516-3516(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;
RA Pauken C.M., Nagle D.L., Bucan M., Lo C.W.;
RT "Molecular cloning, expression analysis, and chromosomal localization
RL of mouse Hmg1-containing sequences.";
RL Mamm. Genome 5:91-99(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=129/SV; TISSUE=Liver;
RC MEDLINE=95050689; PubMed=7961836;
RA Ferrari S., Ronfani L., Calogero S., Bianchi M.;
RT "The mouse gene coding for high mobility group 1 protein (HMG1).";
RL J. Biol. Chem. 269:28803-28808(1994).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AKR/J;
RA Ghosh B.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Maman A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzowski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC double stranded DNA. Heparin-binding protein that has a role in
CC the extension of neurite-type cytoplasmic processes in developing
CC cells.
CC -!- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated
CC with the plasma membrane of filipodia in process-growing cells,
CC and also deposited into the substrate-attached material.
CC -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Z11997; CA478042.1; -; mRNA.
DR EMBL; U00431; AAA20508.1; -; mRNA.
DR EMBL; X80457; CAAS6631.1; -; Genomic DNA.
DR EMBL; L38477; AAA57042.1; -; mRNA.
DR EMBL; BC006586; AAH0586.1; -; mRNA.
DR EMBL; BC008565; AAH08565.1; -; mRNA.
DR EMBL; BC083667; AAH83667.1; -; mRNA.
DR EMBL; BC085090; AAH85090.1; -; mRNA.
DR PIR; I48688; I48688.
DR SMR; P63158; 1-83, 92-170.
DR MGI; MGI:96113; Hmgbl.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0006810; P:transport; IDA.
DR InterPro; IPR000135; Highmoblty_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBLTY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS01118; HMG_BOX_2; 2.
KW Chromosomal protein; DNA-binding; Heparin-binding; Nuclear protein;
KW Repeat.
FT INIT MET 0 0 By similarity.
FT DNA_BIND 8 78 HMG box 1.
FT DNA_BIND 94 162 HMG box 2.
FT COMPLETAS 185 214 Asp/Glu-rich (acidic).
FT CONFLICT 178 178 E -> V (in Ref. 4).
FT CONFLICT 189 189 D -> E (in Ref. 3).
SQ SEQUENCE 214 AA; 24763 MW; B3C6A91ED6F1B133 CRC64;

Query Match 87.0%; Score 187; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.7e-159;

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Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GKGDPPKPRGKMSSYAFFVOTCRBEEHKKHPDASVNFSFKSCSRWKTMSAKEKGKFE 61  
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Db 1 GKGDPPKPRGKMSSYAFFVOTCRBEEHKKHPDASVNFSFKSCSRWKTMSAKEKGKFE 60  
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Qy 62 DMAKADKARYEREMKYIIPPKGETTKKKFDPNAPRPPSAFLFCSEYRPKIKGSHPGLS 121  
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Db 61 DMAKADKARYEREMKYIIPPKGETTKKKFDPNAPRPPSAFLFCSEYRPKIKGSHPGLS 120  
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Qy 122 IGVDAKKLGGMNNTAADDKOPVEKKAALKKEKYEKDIAAYRAKGPDAAKGGVVYKAEKS 181  
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Db 121 IGVDAKKLGGMNNTAADDKOPVEKKAALKKEKYEKDIAAYRAKGPDAAKGGVVYKAEKS 180  
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Qy 182 KKKKEE 188  
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Db 181 KKKKEE 187  
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RESULT 11  
HMGI RAT STANDARD; PRT; 214 AA.

ID HMGI RAT ID HMGI RAT  
AC P63159; P07155; P27109; P27428;  
DT 01-APR-1988 (Rel. 07, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DE High mobility group protein 1 (HMG-1) (High mobility group protein B1)  
DE (Amphoterin) (Heparin-binding protein p30).  
GN Name:Hmgbl; Synonyms:Hmg-1, Hmgl;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=101116;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=liver;  
RX MEDLINE=88067717; PubMed=3694582;  
RA Paonessa G., Frank R., Cortese R.;  
RL "Nucleotide sequence of rat liver HMG1 cDNA.";  
RN Nucleic Acids Res. 15:9077-9077(1987).  
RN [2]  
RN SEQUENCE REVISION.  
RA Bianchi M.;  
RL Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RN NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
RX MEDLINE=91358468; PubMed=1885601;  
RA Merenmies J., Pihlaskari R., Laitinen J., Martiovaara J., Rauvala H.;  
RL "30-kDa heparin-binding protein of brain (amphoterin) involved in  
neutrite outgrowth. Amino acid sequence and localization in the  
filopodia of the advancing plasma membrane";  
RJ J. Biol. Chem. 266:16722-16729(1991).  
RN [4]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=kidney, Prostate, and Testis;  
RG NIH - Mammalian Gene Collection (MGC) project;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.  
RN [5]  
RN PROTEIN SEQUENCE OF 1-20.  
RX MEDLINE=89066894; PubMed=2461949; DOI=10.1083/jcb.107.6.2293;  
RA Rauvala H., Merenmies J., Pihlaskari R., Korhonen M., Huhtala M.L.,  
Panula P.;  
RL "The adhesive and neurite-promoting molecule p30: analysis of the  
amino-terminal sequence and production of antipeptide antibodies that  
detect p30 at the surface of neuroblastoma cells and of brain  
neurons.";  
RJ J. Cell Biol. 107:2293-2305(1988).  
RN [6]  
RN STRUCTURE BY NMR OF 87-164.  
RX MEDLINE=93223672; PubMed=8467791;  
RA Weir H.M., Kraulis P.J., Hill C.S., Raines A.R.C., Laue E.D.,  
Thomas J.O.;

"Structure of the HMG box motif in the B-domain of HMG1.";  
EMBO J. 12:1311-1319(1993).  
[7]  
STRUCTURE BY NMR OF 1-83.  
STRAIN=Sprague-Dawley;  
MEDLINE=96118376; PubMed=8527432;  
RA Thomas J.O., Broadhurst R.W., Raines A.R.C., Grasseer K.D.,  
Thomas J.O., Laue E.D.;  
RL "Structure of the A-domain of HMG1 and its interaction with DNA as  
studied by heteronuclear three- and four-dimensional NMR  
spectroscopy";  
Biochemistry 34:16596-16607(1995).  
CC -1- FUNCTION: Binds preferentially single-stranded DNA and unwinds  
double stranded DNA. Heparin-binding protein that has a role in  
the extension of neurite-type cytoplasmic processes in developing  
cells.  
CC -1- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated  
with the plasma membrane of filopodia in process-growing cells,  
and also deposited into the substrate-attached material.  
CC -1- SIMILARITY: Belongs to the HMG1/HMG2 protein family.  
CC -1- SIMILARITY: Contains 2 HMG box DNA-binding domains.  
-----  
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the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
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DR ENBL; M64986; AAA40729.1; -; mRNA.  
DR ENBL; Y00463; CAA68526.1; -; mRNA.  
DR ENBL; BC061779; AAH61779.1; -; mRNA.  
DR ENBL; BC081839; AAH81839.1; -; mRNA.  
DR ENBL; BC088402; AAH88402.1; -; mRNA.  
DR PIR; A41175; NSRTH1.  
DR PDB; 1AAB; NMR; @=1-83.  
DR PDB; 1CKT; X-ray; A=7-77.  
DR PDB; 1HME; NMR; @=88-164.  
DR PDB; 1HMF; NMR; @=88-164.  
DR SMR; P63159; 1-83, 92-170.  
DR Ensembl; ENSNR000000030351; Rattus norvegicus.  
DR RGD; 2802; Hmgbl  
DR InterPro; IPR000135; Highmobility\_12.  
DR InterPro; IPR000910; HMG\_12\_box.  
DR Pfam; PF00505; HMG box; 2.  
DR PRINTS; PR00886; HIGHMOBLTY12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS00353; HMG\_BOX\_1; 1.  
DR PROSITE; PS50118; HMG\_BOX\_2; 2.  
KW 3D-structure; Chromosomal protein; Direct protein sequencing;  
KW DNA-binding; Heparin-binding; Nuclear protein; Repeat.  
FT INIT MET; 0  
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FT DNA\_BIND 94 162 HMG box 2.  
FT COMPBIAS 185 214 Asp/Glu-rich (acidic).  
FT HELIX 14 29  
FT TURN 31 32  
FT HELIX 37 49  
FT TURN 50 50  
FT TURN 53 55  
FT HELIX 57 74  
FT TURN 75 76  
FT HELIX 100 115  
FT TURN 117 118  
FT HELIX 121 134  
FT HELIX 137 158  
FT TURN 159 160  
SQ SEQUENCE 214 AA; 24763 MW; B3C6A91FD6F1B133 CRC64;

Query Match 87.0%; Score 187; DB 1; Length 214;  
Best Local Similarity 100.0%; Pred. No. 1.7e-159; Indels 0; Gaps 0;  
Matches 187; Conservative 0; Mismatches 0;

Qy 2 GKGDPPKPRGKMSSYAFFVOTCRBEEHKKHPDASVNFSFKSCSRWKTMSAKEKGKFE 61  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 GKGDPPKPRGKMSSYAFFVOTCRBEEHKKHPDASVNFSFKSCSRWKTMSAKEKGKFE 60  
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Qy 62 DMAKADKARYEREMKYIIPPKGETTKKKFDPNAPRPPSAFLFCSEYRPKIKGSHPGLS 121  
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Db 61 DMAKADKARYEREMKYIIPPKGETTKKKFDPNAPRPPSAFLFCSEYRPKIKGSHPGLS 120  
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Qy 122 IGVDAKKLGGMNNTAADDKOPVEKKAALKKEKYEKDIAAYRAKGPDAAKGGVVYKAEKS 181  
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Qy 182 KKKKEE 188  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 181 KKKKEE 187  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11  
HMGI RAT STANDARD; PRT; 214 AA.

ID HMGI RAT ID HMGI RAT  
AC P63159; P07155; P27109; P27428;  
DT 01-APR-1988 (Rel. 07, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DE High mobility group protein 1 (HMG-1) (High mobility group protein B1)  
DE (Amphoterin) (Heparin-binding protein p30).  
GN Name:Hmgbl; Synonyms:Hmg-1, Hmgl;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=101116;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=liver;  
RX MEDLINE=88067717; PubMed=3694582;  
RA Paonessa G., Frank R., Cortese R.;  
RL "Nucleotide sequence of rat liver HMG1 cDNA.";  
RN Nucleic Acids Res. 15:9077-9077(1987).  
RN [2]  
RN SEQUENCE REVISION.  
RA Bianchi M.;  
RL Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RN NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
RX MEDLINE=91358468; PubMed=1885601;  
RA Merenmies J., Pihlaskari R., Laitinen J., Martiovaara J., Rauvala H.;  
RL "30-kDa heparin-binding protein of brain (amphoterin) involved in  
neurite outgrowth. Amino acid sequence and localization in the  
filopodia of the advancing plasma membrane";  
RJ J. Biol. Chem. 266:16722-16729(1991).  
RN [4]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=kidney, Prostate, and Testis;  
RG NIH - Mammalian Gene Collection (MGC) project;<

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Db 1 GKGDPPKPRGKMSYAFVQTCREHKKKCHPDASVNFSEFSKCSERWKTMSAKEKGF 60
Qy 62 DMAKADKARYEREMKTYIPPKGETKKFKPDNAPKRPSPAPFLFCSEYRPKIKGEHPGLS 121
Db 61 DMAKADKARYEREMKTYIPPKGETKKFKPDNAPKRPSPAPFLFCSEYRPKIKGEHPGLS 120
Qy 122 IGDVAKKLGEMWNNTAADDKQPYEKAALKEKYEKDIAAYRAKGPDAKKGVVKAES 181
Db 121 IGDVAKKLGEMWNNTAADDKQPYEKAALKEKYEKDIAAYRAKGPDAKKGVVKAES 180
Qy 182 KKKKEEE 188
Db 181 KKKKEEE 187

RESULT 12
ID QBENMO MOUSE PRELIMINARY; PRT; 181 AA.
AC QBENMO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:C430013W12 product:high mobility group box 1, full
DE insert sequence. (Fragment).
GN Name:Hmgbl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Haasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
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RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK082902; BAC38678.1; -; mRNA.
DR HSP; P07156; INHN.
DR SMR; QBENMO; 2-84, 93-171.
DR MGI; MGI:96113; Hmgbl.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0030325; P:nitric-oxide synthase regulator activity; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0006910; P:transport; IDA.
DR InterPro; IPR000135; Highmobility 12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBLTY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS00118; HMG_BOX_2; 2.
FT NON TER 181
SQ SEQUENCE 181 AA; 20648 MW; B31D82055FD80D52 CRC64;
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Best Local Similarity 100.0%; Pred. No. 3.6e-154;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSYAFVQTCREHKKKCHPDASVNFSEFSKCSERWKTMSAKEKGF 60
Db 1 MGKGDPPKPRGKMSYAFVQTCREHKKKCHPDASVNFSEFSKCSERWKTMSAKEKGF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKFKPDNAPKRPSPAPFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKFKPDNAPKRPSPAPFLFCSEYRPKIKGEHPGL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKAALKEKYEKDIAAYRAKGPDAKKGVVKAES 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKAALKEKYEKDIAAYRAKGPDAKKGVVKAES 180

Qy 181 S 181
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Db 181 S 181

RESULT 13

Q8C7C4 MOUSE PRELIMINARY; PRT; 178 AA.

AC Q8C7C4

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:G920030E14 product:high mobility group box 1, full insert sequence. (Fragment).

DE Name=Hmgbl;

GN NCBI\_TaxID=10090;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fushiki Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gotojori T., Bono H., Kasukawa T., Saito R., Adachi K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [5]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayaashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka I., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK050659; BAC34367.1; -; mRNA.

DR HSSP; P07156; 1NHN.

DR SMR; Q8C7C4; 2-84, 93-171.

DR MGI; MGI:96113; Hmgbl.

DR GO; GO:0005615; C:extracellular space; IDA.

DR GO; GO:0005634; C:nucleus; TAS.

DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.

DR GO; GO:0006810; P:transport; IDA.

DR InterPro; IPR000135; Highmobility\_12.

DR InterPro; IPR000910; HMG\_12\_box.

DR Pfam; PF00505; HMG\_box; 2.

DR PRINTS; PR00886; HIGHMOBILITY12.

DR SMART; SM00398; HMG; 2.

DR PROSITE; PS00353; HMG\_BOX\_1; 1.

DR PROSITE; PS01118; HMG\_BOX\_2; 2.

FT NON TER 178 178

SQ SEQUENCE 178 AA; 20303 MW; 155FDD8D52960A62 CRC64;

Query Match 82.8%; Score 178; DB 2; Length 178;

Best Local Similarity 100.0%; Pred. No. 1.7e-151;

Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKGDPKPKGRKMSSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWMTMSAKGKGF 60

DB 1 MGKGDPKPKGRKMSSYAFFVQTCREHKKKHPDASVNFSEFSKCSERWMTMSAKGKGF 60

QY 61 EDMAKADKARYEREMKTYIPPKGETKKFKDPNAPRPPSAPFLFCSEVRPKIKGSHPG 120

DB 61 EDMAKADKARYEREMKTYIPPKGETKKFKDPNAPRPPSAPFLFCSEVRPKIKGSHPG 120

QY 121 SIGDVAKLGLGEMWNTAADKQPYEKKAAKLEKYEKDIAAVRAKGPDAAKGVVKA 178

DB 121 SIGDVAKLGLGEMWNTAADKQPYEKKAAKLEKYEKDIAAVRAKGPDAAKGVVKA 178

RESULT 14

Q9QX40 SPAEH PRELIMINARY; PRT; 215 AA.

AC Q9QX40;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE High mobility group protein.

DE Name=HMG1;

OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

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OC Muridae; Spalacinae; Nannospalax.
OX NCBI_TaxID=30637;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee K.-L.D., Lum H.-K., Nevo E.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF078920; AAC27653.2; -; Genomic_DNA.
DR HSSP; P07156; INHN.
DR SNR; Q9QX40; 2-84, 93-171.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBLTY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS0118; HMG_BOX_2; 2.
DR PROSITE; PS0118; HMG_BOX_2; 2.
SQ SEQUENCE 215 AA; 24895 MW; 599FB8A6DF41F17 CRC64;

Query Match 74.4%; Score 160; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 3e-135;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 EKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKG 115
Db 56 EKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKG 115

QY 116 EHPGLSIGDVAKLGEWMNNTAADDKQPYEKKAKLKEKYEKDIAYRAKGPDAKKG 175
Db 116 EHPGLSIGDVAKLGEWMNNTAADDKQPYEKKAKLKEKYEKDIAYRAKGPDAKKG 175

QY 176 VKAEKSKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 176 VKAEKSKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 15
Q5T7C2 HUMAN
ID Q5T7C2_HUMAN PRELIMINARY; PRT; 157 AA.
AC Q5T7C2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE High-mobility group box 1 (Fragment).
GN Name=HMGBl; ORFNames=RP11-550P23.1-009;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL353648; CAI15604.1; -; Genomic_DNA.
DR SNR; Q5T7C2; 2-84, 89-157;
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBLTY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS0118; HMG_BOX_2; 2.
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 18164 MW; F38343E7F52FC457 CRC64;
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Query Match 73.0%; Score 157; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e-132;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKGDPKKPRGKMSSYAFFVQTCREBHKKGHPDASVNFSEFSKKCSERWKTMSAKKGF 60
Db 1 MGKGDPKKPRGKMSSYAFFVQTCREBHKKGHPDASVNFSEFSKKCSERWKTMSAKKGF 60

QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120

QY 121 SIGDVAKLGEWMNNTAADDKQPYEKKAKLKEKYEK 157
Db 121 SIGDVAKLGEWMNNTAADDKQPYEKKAKLKEKYEK 157

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Job time : 231 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:40:58 ; Search time 46 Seconds  
(without alignments)  
386.419 Million cell updates/sec

Title: US-10-717-984-1  
Perfect score: 215  
Sequence: 1 MGRGDPKPRGKMSYAFFV.....DEEEDEDEDEEDDDDE 215

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 1

Total number of hits satisfying chosen parameters: 570988

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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2: /cgm2\_6/ptodata/1/iaa/6 COMB.pap.\*  
3: /cgm2\_6/ptodata/1/iaa/H COMB.pap.\*  
4: /cgm2\_6/ptodata/1/iaa/PCTUS COMB.pap.\*  
5: /cgm2\_6/ptodata/1/iaa/RE COMB.pap.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	214	99.5	214	2	US-09-538-092-883
2	214	99.5	214	2	US-09-214-881A-1
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4	140	65.1	214	2	US-09-214-881A-4
5	140	65.1	214	2	US-09-214-881A-5
6	98	45.6	101	2	US-09-513-999C-7904
7	92	42.8	213	2	US-09-949-016-10813
8	90	41.9	110	2	US-09-513-999C-4824
9	61	28.4	110	2	US-09-513-999C-4825
10	39	18.1	59	2	US-09-513-999C-4826
11	30	14.0	30	1	US-08-803-545-1
12	26	12.1	208	2	US-09-538-092-1018
13	26	12.1	208	2	US-09-214-881A-2
14	26	12.1	209	2	US-09-214-881A-6
15	26	12.1	209	2	US-09-214-881A-8
16	26	12.1	320	2	US-09-949-016-10728
17	22	10.2	208	2	US-09-214-881A-11
18	22	10.2	879	2	US-09-914-259-38
19	21	9.8	32	2	US-09-214-881A-13
20	19	8.8	206	2	US-09-214-881A-9
21	18	8.4	18	1	US-08-630-645-11
22	18	8.4	18	2	US-08-766-596A-11
23	18	8.4	18	4	PCT-US96-10220-11
24	16	7.4	185	2	US-09-214-881A-7
25	15	7.0	16	1	US-08-036-555B-8
26	15	7.0	16	1	US-08-469-569-8
27	15	7.0	16	1	US-08-249-322A-8

28	15	7.0	16	1	US-08-469-526A-8	Sequence 8, Appli
29	15	7.0	16	1	US-08-734-591A-8	Sequence 8, Appli
30	15	7.0	16	1	US-08-469-560-8	Sequence 8, Appli
31	15	7.0	16	2	US-08-470-325-8	Sequence 8, Appli
32	15	7.0	16	2	US-08-735-021-8	Sequence 8, Appli
33	15	7.0	16	2	US-08-734-664A-8	Sequence 8, Appli
34	15	7.0	16	2	US-08-470-339-8	Sequence 8, Appli
35	15	7.0	16	2	US-08-467-602-8	Sequence 8, Appli
36	15	7.0	16	4	PCT-US94-05083C-8	Sequence 8, Appli
37	15	7.0	16	4	PCT-US95-08846A-8	Sequence 8, Appli
38	15	7.0	32	2	US-09-214-881A-12	Sequence 12, Appli
39	15	7.0	122	2	US-09-513-999C-4966	Sequence 4966, Ap
40	15	7.0	200	2	US-09-702-705-324	Sequence 324, App
41	15	7.0	200	2	US-09-702-705-789	Sequence 789, App
42	15	7.0	200	2	US-09-736-457-324	Sequence 324, App
43	15	7.0	200	2	US-09-736-457-789	Sequence 789, App
44	15	7.0	200	2	US-09-614-124B-324	Sequence 324, App
45	15	7.0	200	2	US-09-614-124B-789	Sequence 789, App

## ALIGNMENTS

RESULT 1  
US-09-538-092-883  
; Sequence 883, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Mansfield, Traci A.  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CurapatSeqFormatter Version 0.9  
; SEQ ID NO 883  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Polypeptide Accession Number P09429  
US-09-538-092-883

Query Match	99.5%	Score 214;	DB 2;	Length 214;
Best Local Similarity	100.0%;	Pred. No. 2.6e-187;		
Matches 214;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	2	GKGDPPKPRGKMSYAFFVOTCR	EEHKKKHPDASVNFSESKCSERK	WTMSAKEKCKFE 61
Db	1	GKGDPPKPRGKMSYAFFVOTCR	EEHKKKHPDASVNFSESKCSERK	WTMSAKEKCKFE 60
Qy	62	DMAKADKARYEREMKTYIPPKG	ETKKFKDPNAPKRPSPAFFLFC	SEYRPKIKGEHPGLS 121
Db	61	DMAKADKARYEREMKTYIPPKG	ETKKFKDPNAPKRPSPAFFLFC	SEYRPKIKGEHPGLS 120
Qy	122	IGDVAKKGLGEMWNNTAADDKQ	PVEKKAUKLKEYEKDIAAYRAK	GKPDAAKGGVVKAFKS 181
Db	121	IGDVAKKGLGEMWNNTAADDKQ	PVEKKAUKLKEYEKDIAAYRAK	GKPDAAKGGVVKAFKS 180
Qy	182	KKKKEEEDDEDEDEDEDEDEDE	DEDEDEDEDEDEDEDEDEDE	DDDDDE 215
Db	181	KKKKEEEDDEDEDEDEDEDEDE	DEDEDEDEDEDEDEDEDEDE	DDDDDE 214

RESULT 2  
US-09-214-881A-1

```

; Sequence 1, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-1

Query Match          99.5%; Score 214; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.6e-187;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
DB 1 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

QY 62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 121
DB 61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 120

QY 122 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 181
DB 121 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 180

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-214-881A-3

Query Match          95.3%; Score 205; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.2e-179;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
DB 1 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

QY 62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 121
DB 61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 120

QY 122 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 181
DB 121 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 180

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-214-881A-3

Query Match          95.3%; Score 205; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.2e-179;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
DB 1 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

QY 62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 121
DB 61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 120

QY 122 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 181
DB 121 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 180

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-214-881A-3

Query Match          95.3%; Score 205; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.2e-179;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
DB 1 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

QY 62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 121
DB 61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 120

QY 122 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 181
DB 121 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 180

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-214-881A-3

Query Match          95.3%; Score 205; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.2e-179;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
DB 1 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

QY 62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 121
DB 61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 120

QY 122 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 181
DB 121 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 180

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-214-881A-3

Query Match          95.3%; Score 205; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.2e-179;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
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QY 122 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 181
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; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-214-881A-3

Query Match          95.3%; Score 205; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.2e-179;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
DB 1 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

QY 62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 121
DB 61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 120

QY 122 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 181
DB 121 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 180

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-214-881A-3

Query Match          95.3%; Score 205; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.2e-179;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GKGDPKPKRGKSSYAFFVQTCREEHKKKHDPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
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QY 62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 121
DB 61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPSAFFLFCSEYRPKIKGEHPGLS 120

QY 122 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 181
DB 121 IGDVAKKLGE MNNTAADDKQPYEKKAAKLKEKYEKDI AAYRAKGPDAAKG VVKAES 180

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE
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; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214.881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; TYPE: PRT
; LENGTH: 214
; ORGANISM: Rattus rattus
; ORGANISM: Rattus rattus
US-09-214-881A-5

Query Match      65.1%; Score 140; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 7.1e-120;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GKGDPPKPRGKMSYAFFVQTCREHHKKHPPDASVNFSEFSKCSERWKTMSAKEKGKF 61
Db 1 GKGDPPKPRGKMSYAFFVQTCREHHKKHPPDASVNFSEFSKCSERWKTMSAKEKGKF 60

Qy 62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGEHPGLS 121
Db 61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPSPAFFLFCSEYRPKIKGEHPGLS 120

Qy 122 IGDVAKKLGEMWNNTAADDK 141
Db 121 IGDVAKKLGEMWNNTAADDK 140

RESULT 6
US-09-513-999C-7904
; Sequence 7904; Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7904
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-7904

Query Match      45.6%; Score 98; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 7.2e-82;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSYAFFVQTCREHHKKHPPDASVNFSEFSKCSERWKTMSAKEKGKF 60
Db 1 MGKGDPPKPRGKMSYAFFVQTCREHHKKHPPDASVNFSEFSKCSERWKTMSAKEKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRP 98
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRP 98

RESULT 7
US-09-949-016-10813
; Sequence 10813; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10813
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10813

Query Match      42.8%; Score 92; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 3.9e-76;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 YRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEYEKDIAAYRAKGP 168
Db 111 YRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEYEKDIAAYRAKGP 170

Qy 169 DAAKGVVKAESKKKKEEEDDEDEEE 200
Db 171 DAAKGVVKAESKKKKEEEDDEDEEE 202

RESULT 8
US-09-513-999C-4824
; Sequence 4824; Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4824
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 91
; OTHER INFORMATION: Xaa=Asp or Gly
US-09-513-999C-4824

Query Match      41.9%; Score 90; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKMSYAFFVQTCREHHKKHPPDASVNFSEFSKCSERWKTMSAKEKGKF 60
Db 1 MGKGDPPKPRGKMSYAFFVQTCREHHKKHPPDASVNFSEFSKCSERWKTMSAKEKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFK 90
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFK 90

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RESULT 9
US-09-513-999C-4825
; Sequence 4825, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4825
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 12
; OTHER INFORMATION: Xaa=Glu or Lys
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 17
; OTHER INFORMATION: Xaa=Ala or Gly
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 29
; OTHER INFORMATION: Xaa=Lys or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 91
; OTHER INFORMATION: Xaa=Asp or Gly
US-09-513-999C-4825

Query Match      28.4%; Score 61; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 4e-48;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 KHPDASVNFSEFSKCSERWKTMSAKEKGFEDMAKADKARYEREMKTYIPPKGETKKKF 89
Db 30 KHPDASVNFSEFSKCSERWKTMSAKEKGFEDMAKADKARYEREMKTYIPPKGETKKKF 89
Qy 90 K 90
Db 90 K 90

RESULT 10
US-09-513-999C-4826
; Sequence 4826, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4826
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-09-513-999C-4826

Query Match      18.1%; Score 39; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 MSAKEKGKGFEDMAKADKARYEREMKTYIPPKGETKKKF 90
Db 1 MSAKEKGKGFEDMAKADKARYEREMKTYIPPKGETKKKF 39

RESULT 11
US-08-803-545-1
; Sequence 1, Application US/08803545
; Patent No. 5851986
; GENERAL INFORMATION:
; APPLICANT: TAKADA, Yukihiro
; APPLICANT: YAMAMURA, Junichi
; APPLICANT: GOTO, Masaaki
; APPLICANT: AOE, Seichiro
; TITLE OF INVENTION: An Agent Promoting Bone Formation and
; TITLE OF INVENTION: Inhibiting Bone Resorption
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,545
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, Paula A.
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FJN-054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-803-545-1

Query Match      14.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GKGDPPKPKRGKMSVYAFVQTCREHKKKH 31
Db 1 GKGDPPKPKRGKMSVYAFVQTCREHKKKH 30

RESULT 12
US-09-538-092-1018
; Sequence 1018, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542

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; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1018
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018

Query Match      12.1%; Score 26; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 5.3e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 KPRGKMSSYAFFVQTCREHKKKHPD 33
Db      7 KPRGKMSSYAFFVQTCREHKKKHPD 32

RESULT 13
US-09-214-881A-2
; Sequence 2, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-2

Query Match      12.1%; Score 26; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 5.3e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 KPRGKMSSYAFFVQTCREHKKKHPD 33
Db      7 KPRGKMSSYAFFVQTCREHKKKHPD 32

RESULT 14
US-09-214-881A-6
; Sequence 6, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-214-881A-6

Query Match      12.1%; Score 26; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 5.3e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 KPRGKMSSYAFFVQTCREHKKKHPD 33
Db      7 KPRGKMSSYAFFVQTCREHKKKHPD 32

RESULT 15
US-09-214-881A-8
; Sequence 8, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-214-881A-8

Query Match      12.1%; Score 26; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 5.3e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 KPRGKMSSYAFFVQTCREHKKKHPD 33
Db      7 KPRGKMSSYAFFVQTCREHKKKHPD 32

Search completed: April 6, 2006, 10:42:22
Job time : 47 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:41:43 ; Search time 167 Seconds  
(without alignments)  
537.924 Million cell updates/sec

Title: US-10-717-984-1

Perfect score: 215

Sequence: 1 MGKGDPPKRGKSSYAFFV.....DEEEDEDEDEDEDDDE 215

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Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829336 residues

Word size : 1

Total number of hits satisfying chosen parameters: 1866650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:\*

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- 2: /cgn2\_6/ptodata/1/pubpa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	215	100.0	215	4	US-10-087-192-1446
2	215	100.0	215	4	US-10-147-447-1
3	215	100.0	215	4	US-10-300-072-1
4	215	100.0	215	4	US-10-456-949-1
5	215	100.0	215	4	US-10-456-947-1
6	215	100.0	215	4	US-10-718-495-1
7	215	100.0	215	4	US-10-717-984-1
8	215	100.0	215	5	US-10-868-577A-63
9	215	100.0	215	5	US-10-868-549-22
10	215	100.0	215	5	US-10-938-992-74
11	214	99.5	214	3	US-09-214-881A-1
12	214	99.5	214	5	US-10-726-195-1
13	214	99.5	221	5	US-10-938-992-40
14	206	95.8	215	5	US-10-938-992-38
15	205	95.3	214	3	US-09-214-881A-3
16	205	95.3	214	5	US-10-726-195-3
17	188	87.4	215	4	US-10-147-447-2
18	188	87.4	215	4	US-10-300-072-2
19	188	87.4	215	4	US-10-456-949-2
20	188	87.4	215	4	US-10-456-947-2
21	188	87.4	215	4	US-10-718-495-2
22	188	87.4	215	4	US-10-717-984-2
23	188	87.4	215	5	US-10-938-992-18
24	188	87.4	220	4	US-10-087-192-1443
25	188	87.4	252	5	US-10-938-992-5
26	156	72.6	178	4	US-10-264-049-3323
27	153	71.2	180	5	US-10-938-992-36

28	147	68.4	176	4	US-10-094-749-2948	Sequence 2948, Ap
29	141	65.6	215	5	US-10-938-992-37	Sequence 37, Appl
30	140	65.1	214	3	US-09-214-881A-4	Sequence 4, Appli
31	140	65.1	214	3	US-09-214-881A-5	Sequence 5, Appli
32	140	65.1	214	5	US-10-726-195-4	Sequence 5, Appli
33	140	65.1	214	5	US-10-726-195-5	Sequence 5, Appli
34	137	63.7	215	6	US-11-013-684-17	Sequence 17, Appl
35	118	54.9	128	3	US-09-925-300-1757	Sequence 1757, Ap
36	117	54.4	121	3	US-09-925-299-1055	Sequence 1055, Ap
37	117	54.4	121	3	US-09-925-299-1055	Sequence 1055, Ap
38	116	54.0	128	4	US-10-106-698-6757	Sequence 6757, Ap
39	108	50.2	216	4	US-10-147-447-18	Sequence 18, Appl
40	108	50.2	216	4	US-10-300-072-18	Sequence 24, Appl
41	108	50.2	216	4	US-10-300-072-24	Sequence 24, Appl
42	108	50.2	216	4	US-10-456-949-18	Sequence 18, Appl
43	108	50.2	216	4	US-10-456-947-6	Sequence 6, Appli
44	108	50.2	216	4	US-10-456-947-10	Sequence 10, Appl
45	108	50.2	216	4	US-10-718-495-18	Sequence 18, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-087-192-1446  
; Sequence 1446, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; FILE OF INVENTION: CANCER  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1446  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-087-192-1446

Query Match	100.0%;	Score 215;	DB 4;	Length 215;
Best Local Similarity	100.0%;	Pred. No. 6e-173;		
Matches 215;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGKGDPPKRGKSSYAFFVQTCREHKKKHDPDASVNFSEFSKCSRWKTSKAKGKF	60	
Db	1	MGKGDPPKRGKSSYAFFVQTCREHKKKHDPDASVNFSEFSKCSRWKTSKAKGKF	60	
Qy	61	EDMAKADKARYEREMKTYIPPKGETKKKPDNAPKPPSAFFLFCSEYRPKIGEHPL	120	
Db	61	EDMAKADKARYEREMKTYIPPKGETKKKPDNAPKPPSAFFLFCSEYRPKIGEHPL	120	
Qy	121	SIGDVAKLCEMNNNTAADKQVYEKKAALKKEYEKIDIAAYRAKGPDAKKGWKAEK	180	
Db	121	SIGDVAKLCEMNNNTAADKQVYEKKAALKKEYEKIDIAAYRAKGPDAKKGWKAEK	180	
Qy	181	SKKKKEEEDDE	215	
Db	181	SKKKKEEEDDE	215	

##### RESULT 2

US-10-147-447-1  
; Sequence 1, Application US/10147447  
; Publication No. US20030060410A1  
; GENERAL INFORMATION:



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; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-456-947-1

Query Match      100.0%; Score 215; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTSKKEGKF 60
Db 1 MGKGDPPKPRGKSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTSKKEGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120

Qy 121 SIGDVAKKLGEMWNTAADKQPYEKKAALKKEYEKDIAAYRAKGPDAKKGWVKAEK 180
Db 121 SIGDVAKKLGEMWNTAADKQPYEKKAALKKEYEKDIAAYRAKGPDAKKGWVKAEK 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 6
US-10-718-495-1
; Sequence 1, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
; FILE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3258.1009-001
; CURRENT APPLICATION NUMBER: US/10718,495
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/427,841
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-718-495-1

Query Match      100.0%; Score 215; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTSKKEGKF 60
Db 1 MGKGDPPKPRGKSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTSKKEGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120

Qy 121 SIGDVAKKLGEMWNTAADKQPYEKKAALKKEYEKDIAAYRAKGPDAKKGWVKAEK 180
Db 121 SIGDVAKKLGEMWNTAADKQPYEKKAALKKEYEKDIAAYRAKGPDAKKGWVKAEK 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
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RESULT 7
US-10-717-984-1
; Sequence 1, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
; FILE REFERENCE: 3258.1008-001
; CURRENT APPLICATION NUMBER: US/10717,984
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,846
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-717-984-1

Query Match      100.0%; Score 215; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTSKKEGKF 60
Db 1 MGKGDPPKPRGKSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTSKKEGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120

Qy 121 SIGDVAKKLGEMWNTAADKQPYEKKAALKKEYEKDIAAYRAKGPDAKKGWVKAEK 180
Db 121 SIGDVAKKLGEMWNTAADKQPYEKKAALKKEYEKDIAAYRAKGPDAKKGWVKAEK 180

Qy 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 8
US-10-868-577A-63
; Sequence 63, Application US/10868577A
; Publication No. US20050032697A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-577A-63

Query Match      100.0%; Score 215; DB 5; Length 215;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPPKPRGKSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTSKKEGKF 60
Db 1 MGKGDPPKPRGKSSYAFFVQTCREHHKKHPPDASVNFSEFSKCSRWKTSKKEGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPPSAFFLFCSEYRPKIKGEHPGL 120
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[illegible]

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RESULT 9
US-10-868-549-22
; Sequence 22, Application US/10868549
; Publication No. US20050043235A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY
; FILE REFERENCE: 28967/39117A
; CURRENT APPLICATION NUMBER: US/10/868,549
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,114
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 215
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-868-549-22

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Query Match	100.0%	Score 215;	DB 5;	Length 215;
Best Local Similarity	100.0%;	Pred. No. 6e-173;		
Matches 215; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	MGKGDPKPKPGKWSSYAFFVQTCEEHKKKHDPASVNFSEFKCSERWKTMSAKEGKF	60	
Db	1	MGKGDPKPKPGKWSSYAFFVQTCEEHKKKHDPASVNFSEFKCSERWKTMSAKEGKF	60	
Qy	61	EDMAKDARYEREMKTYIIPPKGTTKKCFDNPAPKPSPSAPFFLFCSEYRPKI KGEHPGL	120	
Db	61	EDMAKDARYEREMKTYIIPPKGTTKKCFDNPAPKPSPSAPFFLFCSEYRPKI KGEHPGL	120	
Qy	121	SIGDVAKLGEMWNNTAADKQPVEKKAALKKEYEKDIAAYRAKGKPDAAKGGVWAEK	180	
Db	121	SIGDVAKLGEMWNNTAADKQPVEKKAALKKEYEKDIAAYRAKGKPDAAKGGVWAEK	180	
Qy	181	SKKKKEEDEDDEDEEEDEDEDEDEDEDDDDDE	215	
Db	181	SKKKKEEDEDDEDEEEDEDEDEDEDEDDDDDE	215	

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RESULT 10
US-10-938-992-74
; Sequence 74, Application US/10938992
; Publication NO. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Char, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74

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; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-992-74

Query Match      100.0%; Score 215, DB 5; Length 215;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1  MGKGDPKPKRGKMSSYAFFVQTCEEHKKKHGPDAASVNFSEFSKCSERWKTMSAKEGKF  60
     ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1  MGKGDPKPKRGKMSSYAFFVQTCEEHKKKHGPDAASVNFSEFSKCSERWKTMSAKEGKF  60

Qy   61 EDMAKDARYEREMKTYIIPKGETKKFKPDNPAPKPSPPSAFPLFCSEYRPKIAGEHPGL  120
     ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   61 EDMAKDARYEREMKTYIIPKGETKKFKPDNPAPKPSPPSAFPLFCSEYRPKIAGEHPGL  120

Qy   121 SIGDVAKKLGE MNNTAADDQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKGGVVAEK  180
     ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   121 SIGDVAKKLGE MNNTAADDQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKGGVVAEK  180

Qy   181 SKKKKGEEDDEDEEEEDDEDEDEDEDEDDDE  215
Db   181 SKKKKGEEDDEDEEEEDDEDEDEDEDEDDDE  215
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RESULT 11
US-09-214-881A-1
; Sequence 1, Application US/09214881A
; Patent No. US2002009749A1
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214.881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-214-881A-1

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[illegible]



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RESULT 12
US-10-726-195-1
; Sequence 1, Application US/10726195
; Publication No. US20040229279A1
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Useugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuo
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Okakada, Runio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/10726,195
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US/09/214,881A
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-195-1

Query Match      99.5%; Score 214; DB 5; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.2e-172;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  GKGDPPKPRGKMSYAFFVQTCREHHKKHPDASVNFSEFSKCCSERWKTMSAKEKGKFE 61
Db   1  GKGDPPKPRGKMSYAFFVQTCREHHKKHPDASVNFSEFSKCCSERWKTMSAKEKGKFE 60

QY  62  DMAKADKARYEREMKTYIPPKGETKKKFDPNAPKRPSPAFFLFCSEYRPKIKGEHPGLS 121
Db   61  DMAKADKARYEREMKTYIPPKGETKKKFDPNAPKRPSPAFFLFCSEYRPKIKGEHPGLS 120

QY  122  IGDVAKKLGEMWNTAADDKQPYEKKAAKLKEYEKDIAAYRAKGPDAAKKGWVKAES 181
Db   121  IGDVAKKLGEMWNTAADDKQPYEKKAAKLKEYEKDIAAYRAKGPDAAKKGWVKAES 180

QY  182  KKKKEEEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db   181  KKKKEEEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 214

RESULT 13
US-10-938-992-40
; Sequence 40, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rec-HMGB1-His6
US-10-938-992-40

Query Match      99.5%; Score 214; DB 5; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.2e-172;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  GKGDPPKPRGKMSYAFFVQTCREHHKKHPDASVNFSEFSKCCSERWKTMSAKEKGKFE 61
Db   1  GKGDPPKPRGKMSYAFFVQTCREHHKKHPDASVNFSEFSKCCSERWKTMSAKEKGKFE 60

QY  62  DMAKADKARYEREMKTYIPPKGETKKKFDPNAPKRPSPAFFLFCSEYRPKIKGEHPGLS 121
Db   61  DMAKADKARYEREMKTYIPPKGETKKKFDPNAPKRPSPAFFLFCSEYRPKIKGEHPGLS 120

QY  122  IGDVAKKLGEMWNTAADDKQPYEKKAAKLKEYEKDIAAYRAKGPDAAKKGWVKAES 181
Db   121  IGDVAKKLGEMWNTAADDKQPYEKKAAKLKEYEKDIAAYRAKGPDAAKKGWVKAES 180

QY  182  KKKKEEEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db   181  KKKKEEEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 214

RESULT 14
US-10-938-992-38
; Sequence 38, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-938-992-38

Query Match      95.8%; Score 206; DB 5; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.3e-165;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  MGKGDPPKPRGKMSYAFFVQTCREHHKKHPDASVNFSEFSKCCSERWKTMSAKEKGKFE 60
Db   1  MGKGDPPKPRGKMSYAFFVQTCREHHKKHPDASVNFSEFSKCCSERWKTMSAKEKGKFE 60

QY  61  EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKRPSPAFFLFCSEYRPKIKGEHPGL 120
Db   61  EDMAKADKARYEREMKTYIPPKGETKKKFDPNAPKRPSPAFFLFCSEYRPKIKGEHPGL 120

QY  121  SIGDVAKKLGEMWNTAADDKQPYEKKAAKLKEYEKDIAAYRAKGPDAAKKGWVKAES 180
Db   121  SIGDVAKKLGEMWNTAADDKQPYEKKAAKLKEYEKDIAAYRAKGPDAAKKGWVKAES 180

QY  181  SKKKKEEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 206
Db   181  SKKKKEEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 206

RESULT 15
US-09-214-881A-3
; Sequence 3, Application US/09214881A
; Patent No. US20020009749A1
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
```

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; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-214-881A-3

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Query Match          95.3%; Score 205; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.6e-164;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  GKGDPPKPRGKMSYAFFVOTCREHHKKHPDASVNFSPFSKCSERWKTMSAKEKGKPE 61
Db      1  GKGDPPKPRGKMSYAFFVOTCREHHKKHPDASVNFSPFSKCSERWKTMSAKEKGKPE 60

Qy      62  DMAKADKARYEREMKTYIPKGETKKKFPDNPAPKPPPSAFLFCSEYRPKIKGEHPGLS 121
Db      61  DMAKADKARYEREMKTYIPKGETKKKFPDNPAPKPPPSAFLFCSEYRPKIKGEHPGLS 120

Qy      122  IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEYEKDIAAYRAKGPDAAKGKGVVKAES 181
Db      121  IGDVAKKLGEMWNNTAADDKQPYEKKAALKKEYEKDIAAYRAKGPDAAKGKGVVKAES 180

Qy      182  KKKKEEEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 206
Db      181  KKKKEEEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 205

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Job time : 168 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 10:42:38 ; Search time 24 Seconds  
(without alignments)  
279.428 Million cell updates/sec

Title: US-10-717-984-1  
Perfect score: 215  
Sequence: 1 MGKGDPPKPRGKSSYAFFV.....DEREEDEDEDEDDDE 215

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 184161 seqs, 31191982 residues

Word size : 1

Total number of hits satisfying chosen parameters: 184041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:\*  
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2: /SID55/ptodata/2/pubpaa/US06 NEW PUB.pap.\*  
3: /SID55/ptodata/2/pubpaa/US07 NEW PUB.pap.\*  
4: /SID55/ptodata/2/pubpaa/PCT NEW PUB.pap.\*  
5: /SID55/ptodata/2/pubpaa/US09 NEW PUB.pap.\*  
6: /SID55/ptodata/2/pubpaa/US10 NEW PUB.pap.\*  
7: /SID55/ptodata/2/pubpaa/US11 NEW PUB.pap.\*  
8: /SID55/ptodata/2/pubpaa/US60 NEW PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	215	100.0	215	6	US-10-821-234-1443
2	215	100.0	215	7	US-11-186-422-11
3	188	87.4	215	7	US-11-186-422-12
4	69	32.1	69	7	US-11-186-422-14
5	54	25.1	54	6	US-10-719-150-6
6	54	25.1	54	7	US-11-186-422-13
7	22	10.2	879	7	US-11-189-041-192
8	20	9.3	169	6	US-10-821-234-1234
9	14	6.5	14	6	US-10-719-150-1
10	14	6.5	15	6	US-10-719-150-4
11	13	6.0	1163	7	US-11-044-899-2
12	13	6.0	1163	7	US-11-044-899-30
13	13	6.0	1750	7	US-11-087-099-12397
14	12	5.6	447	7	US-11-096-568A-28367
15	10	4.7	106	7	US-11-096-568A-6675
16	10	4.7	417	7	US-11-087-099-12021
17	10	4.7	593	7	US-11-040-488-2
18	10	4.7	1531	6	US-10-330-773-142
19	9	4.2	9	7	US-11-257-286-18
20	9	4.2	106	7	US-11-087-099-7075
21	9	4.2	124	7	US-11-096-568A-9681
22	9	4.2	135	7	US-11-087-099-11504
23	9	4.2	137	7	US-11-096-568A-3511
24	9	4.2	139	7	US-11-096-568A-13611
25	9	4.2	139	7	US-11-096-568A-26884

26	9	4.2	140	7	US-11-172-740-1564	Sequence 1564, Ap
27	9	4.2	141	7	US-11-087-099-3073	Sequence 3073, Ap
28	9	4.2	141	7	US-11-087-099-9185	Sequence 9185, Ap
29	9	4.2	142	7	US-11-087-099-4976	Sequence 4976, Ap
30	9	4.2	144	6	US-10-821-234-1254	Sequence 1254, Ap
31	9	4.2	146	7	US-11-172-740-1569	Sequence 1569, Ap
32	9	4.2	149	7	US-11-087-099-3510	Sequence 3510, Ap
33	9	4.2	149	7	US-11-172-740-1571	Sequence 1571, Ap
34	9	4.2	152	7	US-11-087-099-313	Sequence 313, App
35	9	4.2	152	7	US-11-172-740-1565	Sequence 1565, Ap
36	9	4.2	152	7	US-11-172-740-1566	Sequence 1566, Ap
37	9	4.2	154	7	US-11-087-099-2474	Sequence 2474, Ap
38	9	4.2	154	7	US-11-172-740-1570	Sequence 1570, Ap
39	9	4.2	159	7	US-11-087-099-9017	Sequence 9017, Ap
40	9	4.2	162	7	US-11-096-568A-9680	Sequence 9680, Ap
41	9	4.2	164	7	US-11-096-568A-3510	Sequence 3510, Ap
42	9	4.2	168	7	US-11-233-510-4	Sequence 4, Appli
43	9	4.2	187	7	US-11-096-568A-26883	Sequence 26883, A
44	9	4.2	245	7	US-11-096-568A-28368	Sequence 28368, A
45	9	4.2	291	6	US-10-501-035-245	Sequence 245, App

## ALIGNMENTS

RESULT 1  
US-10-821-234-1443  
; Sequence 1443, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1443  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1443

Query Match 100.0%; Score 215; DB 6; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.3e-192; Indels 0; Gaps 0;  
Matches 215; Conservative 0; Mismatches 0;

Qy 1 MGKGDPPKPRGKSSYAFFVQTCREHKKKHDPASVNFSEFSKCSRWKTSAREKGF 60  
Db 1 MGKGDPPKPRGKSSYAFFVQTCREHKKKHDPASVNFSEFSKCSRWKTSAREKGF 60

Qy 61 EDMAKADKARYEREMKTYIIPKGETKKKFDPNAPKPPSAFFLFCSEYRPKIKEHPGL 120  
Db 61 EDMAKADKARYEREMKTYIIPKGETKKKFDPNAPKPPSAFFLFCSEYRPKIKEHPGL 120

Qy 121 SIGDVAKKLGEMNNTAADDKQYKKAALKKEKYKNDIAAYRAKGPDAKKGVVAEK 180  
Db 121 SIGDVAKKLGEMNNTAADDKQYKKAALKKEKYKNDIAAYRAKGPDAKKGVVAEK 180

Qy 181 SKKKKEEEDDE 215  
Db 181 SKKKKEEEDDE 215

RESULT 2  
US-11-186-422-11  
; Sequence 11, Application US/11186422  
; Publication No. US20060057679A1

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; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186.422
; PRIOR FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-11

Query Match      100.0%; Score 215; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.3e-192;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKGDPPKPRGKSSYAFFVQTCREHKKKHDPDASVNFSEFSKCSRWKTMGAKEGKF 60
Db 1 MGKGDPPKPRGKSSYAFFVQTCREHKKKHDPDASVNFSEFSKCSRWKTMGAKEGKF 60
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120
QY 121 SIGDVAKKLGEMWNNTAADDKQPYEKAALKKEKYEKDIAAYRAKGPDAKKGWVKAEK 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKAALKKEKYEKDIAAYRAKGPDAKKGWVKAEK 180
QY 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 3
US-11-186-422-12
; Sequence 12, Application US/11/186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186.422
; CURRENT FILING DATE: 2005-07-20
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-186-422-12

Query Match      87.4%; Score 188; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-167;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKGDPPKPRGKSSYAFFVQTCREHKKKHDPDASVNFSEFSKCSRWKTMGAKEGKF 60
Db 1 MGKGDPPKPRGKSSYAFFVQTCREHKKKHDPDASVNFSEFSKCSRWKTMGAKEGKF 60
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120

; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186.422
; CURRENT FILING DATE: 2005-07-20
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-13

Query Match      100.0%; Score 215; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.3e-192;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKGDPPKPRGKSSYAFFVQTCREHKKKHDPDASVNFSEFSKCSRWKTMGAKEGKF 60
Db 1 MGKGDPPKPRGKSSYAFFVQTCREHKKKHDPDASVNFSEFSKCSRWKTMGAKEGKF 60
QY 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKPPSAFFLFCSEYRPKIKGEHPGL 120
QY 121 SIGDVAKKLGEMWNNTAADDKQPYEKAALKKEKYEKDIAAYRAKGPDAKKGWVKAEK 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKAALKKEKYEKDIAAYRAKGPDAKKGWVKAEK 180
QY 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Db 181 SKKKKEEEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215

RESULT 4
US-11-186-422-14
; Sequence 14, Application US/11/186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186.422
; CURRENT FILING DATE: 2005-07-20
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-14

Query Match      32.1%; Score 69; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.8e-57;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKAALK 152
Db 1 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKAALK 152
QY 153 EYKEDIAA 161
Db 61 EYKEDIAA 69

RESULT 5
US-10-719-150-6
; Sequence 6, Application US/10719150
; Publication No. US20040120953A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Haichao Wang
; TITLE OF INVENTION: ANTAGONISTS OF HMGI FOR TREATING
; TITLE OF INVENTION: INFLAMMATORY CONDITIONS
; FILE REFERENCE: 3268.1000-011
; CURRENT APPLICATION NUMBER: US/10/719.150
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/10/300.068
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 10/210.747
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 09/503.632
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 09/248.574
; PRIOR FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo Sapiens
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## US-10-719-150-6

Query Match 25.1%; Score 54; DB 6; Length 54;  
Best Local Similarity 100.0%; Pred. No. 2e-43;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 PDASVNFSEFSKCSERWKTSAKEKGKGFEDMAKADKARYEREMKTYIPPKGET 85  
Db 1 PDASVNFSEFSKCSERWKTSAKEKGKGFEDMAKADKARYEREMKTYIPPKGET 54

## RESULT 6

US-11-186-422-13  
; Sequence 13, Application US/11186422  
; Publication No. US20060057679A1  
; GENERAL INFORMATION:  
; APPLICANT: Critical Therapeutics, Inc.  
; APPLICANT: O'Keefe, Theresa  
; APPLICANT: Luciano, Peter  
; APPLICANT: Qin, Shixin  
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES  
; FILE REFERENCE: 3258.1021-003  
; CURRENT APPLICATION NUMBER: US/11/186.422  
; CURRENT FILING DATE: 2005-07-20  
; PRIOR APPLICATION NUMBER: 60/589,678  
; PRIOR FILING DATE: 2004-07-20  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 54  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-186-422-13

Query Match 25.1%; Score 54; DB 7; Length 54;  
Best Local Similarity 100.0%; Pred. No. 2e-43;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 PDASVNFSEFSKCSERWKTSAKEKGKGFEDMAKADKARYEREMKTYIPPKGET 85  
Db 1 PDASVNFSEFSKCSERWKTSAKEKGKGFEDMAKADKARYEREMKTYIPPKGET 54

## RESULT 7

US-11-169-041-192  
; Sequence 192, Application US/11169041  
; Publication No. US20060019284A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF  
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE  
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 10001 NP  
; CURRENT APPLICATION NUMBER: US/11/169.041  
; CURRENT FILING DATE: 2005-06-28  
; PRIOR APPLICATION NUMBER: 60/584,405  
; PRIOR FILING DATE: 2004-06-30  
; NUMBER OF SEQ ID NOS: 527  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 192  
; LENGTH: 879  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-169-041-192

Query Match 10.2%; Score 22; DB 7; Length 879;  
Best Local Similarity 100.0%; Pred. No. 1.4e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 AFFLFCSEYRPKIKGEHPGLSI 122  
Db 775 AFFLFCSEYRPKIKGEHPGLSI 796

## RESULT 8

US-10-821-234-1234  
; Sequence 1234, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821.234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: Pk SEQ\_genes Version 1.0  
; SEQ ID NO 1234  
; LENGTH: 169  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(169)  
; OTHER INFORMATION: Xaa = any amino acid or nothing  
US-10-821-234-1234

Query Match 9.3%; Score 20; DB 6; Length 169;  
Best Local Similarity 100.0%; Pred. No. 2.3e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 SSVAFFVQTCREHKKKHPD 33  
Db 1 SSVAFFVQTCREHKKKHPD 20

## RESULT 9

US-10-719-150-1  
; Sequence 1, Application US/10719150  
; Publication No. US20040120953A1  
; GENERAL INFORMATION:  
; APPLICANT: Kevin J. Tracey  
; APPLICANT: Haichao Wang  
; TITLE OF INVENTION: ANTAGONISTS OF HMGI FOR TREATING  
; TITLE OF INVENTION: INFLAMMATORY CONDITIONS  
; FILE REFERENCE: 3268.1000-011  
; CURRENT APPLICATION NUMBER: US/10/719.150  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US/10/300,068  
; PRIOR FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: US 10/210,747  
; PRIOR FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US 09/503,632  
; PRIOR FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: US 09/248,574  
; PRIOR FILING DATE: 1999-02-11  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-719-150-1

Query Match 6.5%; Score 14; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GKGDPPKKPRGMSS 15  
Db 1 GKGDPPKKPRGMSS 14

```
RESULT 10
US-10-719-150-4
; Sequence 4, Application US/10719150
; Publication No. US20040120953A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Haichao Wang
; TITLE OF INVENTION: ANTAGONISTS OF HMGI FOR TREATING
; FILE REFERENCE: 3268.1000-011
; CURRENT APPLICATION NUMBER: US/10/719,150
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/10/300,068
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 10/210,747
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 09/503,632
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 09/248,574
; PRIOR FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigen
US-10-719-150-4

Query Match      6.5%; Score 14; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  GKGDPKKPRGKMSS 15
        |||||
DB      1  GKGDPKKPRGKMSS 14

RESULT 11
US-11-044-899-2
; Sequence 2, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-2

Query Match      6.0%; Score 13; DB 7; Length 1163;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      192 EDEDEDEDEDEE 204
        |||||
DB      33 EDEDEDEDEDEE 45

RESULT 12
US-11-044-899-30
; Sequence 30, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1163) at all Xaa position
; OTHER INFORMATION: Xaa = any amino acid
US-11-044-899-30

Query Match      6.0%; Score 13; DB 7; Length 1163;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      192 EDEDEDEDEDEE 204
        |||||
DB      33 EDEDEDEDEDEE 45

RESULT 13
US-11-087-099-12397
; Sequence 12397, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12397
; LENGTH: 1750
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-11-087-099-12397

Query Match      6.0%; Score 13; DB 7; Length 1750;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      196 DEEEDEDEDEDE 208
        |||||
DB      1726 DEEEDEDEDEDE 1738

RESULT 14
US-11-096-568A-28367
; Sequence 28367, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28367
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: Ceres Seq. ID no. 2715782
US-11-096-568A-28367

```

```

Query Match          5.6%; Score 12; DB 7; Length 447;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 190 DEEDEDEDEEE 201
Db 169 DEEDEDEDEEE 180

```

```

RESULT 15
US-11-096-568A-6675
; Sequence 6675, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6675
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(106)
; OTHER INFORMATION: Ceres Seq. ID no. 14316260
US-11-096-568A-6675

```

```

Query Match          4.7%; Score 10; DB 7; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 205 DEEDEDDDD 214
Db 40 DEEDEDDDD 49

```

Search completed: April 6, 2006, 10:45:44  
Job time : 24 secs



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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:12:19 ; Search time 83.7533 Seconds  
(without alignments)  
361.981 Million cell updates/sec

Title: US-10-717-984-5

Perfect score: 370

Sequence: 1 NAPKRPSPFAFLFCSEYRPK.....QPYEKKAALKKEKYEDIAA 69

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1\_Geneseq\_21.\*

2: Geneseqp1980s.\*

3: Geneseqp1990s.\*

4: Geneseqp2000s.\*

5: Geneseqp2001s.\*

6: Geneseqp2002s.\*

7: Geneseqp2003as.\*

8: Geneseqp2003bs.\*

9: Geneseqp2004as.\*

10: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	69	6 AAE35863	Aae35863 HMG1 B box
2	370	100.0	69	8 ADO25922	Ado25922 High mobi
3	370	100.0	69	8 ADO71481	Ado71481 Human/mou
4	370	100.0	74	8 ADO25934	Ado25934 High mobi
5	370	100.0	74	8 ADO71527	Ado71527 Human hig
6	370	100.0	74	9 ADY85362	Ady85362 Human hig
7	370	100.0	74	9 ADY85078	Ady85078 Human HMG
8	370	100.0	74	9 ADY85087	Ady85087 Human HMG
9	370	100.0	75	8 ADR45941	Adr45941 Human hig
10	370	100.0	92	8 ADO25962	Ado25962 High mobi
11	370	100.0	92	8 ADO71534	Ado71534 Human hig
12	370	100.0	92	9 ADY85368	Ady85368 Human hig
13	370	100.0	92	9 ADY85084	Ady85084 Human HMG
14	370	100.0	128	3 AAB57179	Aab57179 Human pro
15	370	100.0	168	8 ABM81641	Abm81641 Tumour-as
16	370	100.0	176	6 ADA55380	Ada55380 Human pro
17	370	100.0	214	7 ADD47645	Add47645 Human pro
18	370	100.0	214	7 ADE60730	Ade60730 Rat Prote
19	370	100.0	214	7 ADE60447	Ade60447 Human pro
20	370	100.0	214	7 ADE57980	Ade57980 Human pro
21	370	100.0	214	7 ADE57984	Ade57984 Human pro
22	370	100.0	214	7 ADE57978	Ade57978 Rat Prote
23	370	100.0	214	7 ADE60732	Ade60732 Human pro
24	370	100.0	214	7 ADE57982	Ade57982 Rat Prote

#### ALIGNMENTS

RESULT 1

AAE35863

ID AAE35863 standard; protein; 69 AA.

XX AAE35863;

AC AAE35863;

XX AAE35863;

DT 17-JUN-2003 (first entry)

XX AAE35863;

DE HMG1 B box.

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

XX AAE35863;

CC The invention relates to high mobility group (HMG) protein comprising DNA  
 CC binding motifs termed HMG A box and HMG B box. HMG A box or a non-  
 CC naturally occurring HMG A box inhibits the release of a pro-inflammatory  
 CC cytokine from a vertebrate cell. The methods and compositions of the  
 CC invention are useful for inhibiting a condition characterised by  
 CC activation of an inflammatory cytokine cascade such as endotoxin shock,  
 CC rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's  
 CC disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,  
 CC sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,  
 CC filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,  
 CC myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout,  
 CC cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host  
 CC disease, diabetes and Hodgkin's disease. The invention is useful in gene  
 CC therapy. The present sequence is HMG1 (also termed as HMGB1) B box found  
 CC in human, mouse and rat  
 XX  
 SQ Sequence 69 AA;

Query Match 100.0%; Score 370; DB 6; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60  
 Db 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60  
 Qy 61 EYKEDIAA 69  
 Db 61 EYKEDIAA 69

RESULT 2  
 ADO25922  
 ID ADO25922 standard; protein; 69 AA.

XX ADO25922;  
 XX  
 XX 26-AUG-2004 (first entry)  
 DT High mobility group box 1 (HMGB1) B box protein sequence.  
 DE  
 XX cytostatic; gene therapy; vaccine; pharmaceutical composition;  
 XX HMGB B box; high mobility group; immune response; immunostimulation;  
 KW cancer; human; mouse; rat; high mobility group box 1; HMGB1;  
 KW cytokine activity; B box.  
 XX  
 OS Mammalia.

XX WO2004046338-A2.  
 XX  
 XX 03-JUN-2004.  
 XX  
 XX 19-NOV-2003; 2003WO-US036975.  
 XX  
 XX 20-NOV-2002; 2002US-0427848P.  
 PR  
 XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 PA  
 XX Tracey KJ;  
 PI  
 XX WPI; 2004-420625/39.  
 DR  
 XX  
 XX New pharmaceutical composition comprises a polypeptide comprising an HMGB  
 PT B box or its functional variant, useful for stimulating or increasing an  
 PT immune response in an individual or for treating cancer in an individual.

XX Disclosure; SEQ ID NO 5; 68pp; English.  
 XX  
 XX The invention describes a pharmaceutical composition comprising a  
 CC polypeptide comprising an HMGB (high mobility group box) B box or its  
 CC functional variant to treat a disease or condition by increasing an  
 CC immune response in an individual administered with the pharmaceutical  
 CC composition. Also described are: an antibody attached to a polypeptide

CC comprising an HMGB B box or its functional variant; stimulating or  
 CC increasing an immune response in an individual in need of  
 CC immunostimulation; and treating cancer in an individual. The composition  
 CC is useful for stimulating or increasing an immune response in an  
 CC individual in need of immunostimulation or for treating cancer in an  
 CC individual. This is the amino acid sequence of human/mouse/rat high  
 CC mobility group box 1 (HMGB1) B box protein sequence that can be used to  
 CC stimulate cytokine activity and increase immune response to assist in  
 CC treating disease.  
 XX  
 SQ Sequence 69 AA;

Query Match 100.0%; Score 370; DB 8; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60  
 Db 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60  
 Qy 61 EYKEDIAA 69  
 Db 61 EYKEDIAA 69

RESULT 3  
 ADO71481  
 ID ADO71481 standard; protein; 69 AA.

XX ADO71481;  
 XX  
 XX 26-AUG-2004 (first entry)  
 DT Human/mouse/rat high mobility group box 1 (HMGB1) B box protein.  
 DE  
 XX Human; mouse; high mobility group box 1 B box; HMGB1 B box; HMGB;  
 KW HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity;  
 KW inflammation; inflammatory cytokine cascade; sepsis; allograft rejection;  
 KW rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;  
 KW chronic obstructive pulmonary disease; psoriasis; pancreatitis;  
 KW peritonitis; burn; myocardial ischaemia; organic ischaemia;  
 KW reperfusion ischaemia; Behcet's disease; graft-versus-host disease;  
 KW Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia; rat.

OS Homo sapiens.  
 OS Mus sp.  
 OS Rattus sp.  
 XX WO2004046345-A2.  
 XX  
 XX 03-JUN-2004.  
 XX  
 XX 20-NOV-2003; 2003WO-US037507.  
 XX  
 XX 20-NOV-2002; 2002US-0427841P.  
 PR  
 XX 20-NOV-2002; 2002US-0427846P.  
 XX  
 XX (CRIT-) CRITICAL THERAPEUTICS INC.  
 PA  
 XX Newman W, O'keefe TL;  
 PI WPI; 2004-420628/39.  
 DR  
 XX New high mobility group box proteins, useful in treating obesity, sepsis,  
 PT rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,  
 PT Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.  
 XX  
 XX Claim 32; SEQ ID NO 5; 113pp; English.

XX The invention relates to a polypeptide comprising a high mobility group  
 CC box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of  
 CC a proinflammatory cytokine from a cell treated with an HMGB protein. The  
 CC invention also relates to a purified preparation of antibodies that

CC specifically bind to the HMGB B box but do not specifically bind to non-B  
 CC box epitopes of HMGB, where the antibodies can inhibit release of a  
 CC proinflammatory cytokine from a cell treated with HMGB, a method for  
 CC effecting weight loss or treating obesity in a patient, a method of  
 CC determining whether a compound inhibits inflammation, a pharmaceutical  
 CC composition comprising an HMGB protein or an antibody that binds to the  
 CC protein, an agent that inhibits TNF biological activity and a method of  
 CC treating a condition in a patient characterised by activation of an  
 CC inflammatory cytokine cascade. Effecting weight loss or treating obesity  
 CC in a patient comprises administering to the patient an amount of the  
 CC polypeptide. The polypeptide, antibodies, composition and methods are  
 CC useful in treating obesity and conditions characterised by activation of  
 CC an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,  
 CC rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,  
 CC chronic obstructive pulmonary disease, psoriasis, pancreatitis,  
 CC peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion  
 CC ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,  
 CC ulcerative colitis, multiple sclerosis or cachexia. This sequence  
 CC represents a human/mouse/rat HMGB1 B box polypeptide of the invention.  
 XX  
 XX Sequence 69 AA;

Query Match 100.0%; Score 370; DB 8; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKPPSAFFLCSEYRPKIKGEHPGLSGDVAKKLGEWMNNTAADDKPYEKKAALK 60  
 DB 1 NAPKPPSAFFLCSEYRPKIKGEHPGLSGDVAKKLGEWMNNTAADDKPYEKKAALK 60  
 QY 61 EYKEDIAA 69  
 DB 61 EYKEDIAA 69

RESULT 4  
 AD025934  
 ID AD025934 standard; peptide; 74 AA.  
 XX  
 AC AD025934;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX High mobility group box 1 B box fragment seqid 17.  
 XX  
 XX cytostatic; gene therapy; vaccine; pharmaceutical composition;  
 KW HMGB B box; high mobility group; immune response; immunostimulation;  
 KW cancer; human; high mobility group box 1; HMGB1; cytokine activity; B box.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2004046338-A2.  
 XX  
 XX 03-JUN-2004.  
 XX  
 XX 19-NOV-2003; 2003WO-US036975.  
 XX  
 XX 20-NOV-2002; 2002US-0427848P.  
 XX  
 XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 XX  
 XX Tracey KJ;  
 XX  
 XX WPI; 2004-420625/39.  
 XX  
 XX New pharmaceutical composition comprises a polypeptide comprising an HMGB  
 PT B box or its functional variant, useful for stimulating or increasing an  
 PT immune response in an individual or for treating cancer in an individual.  
 XX  
 XX Disclosure; SEQ ID NO 17; 68pp; English.  
 XX  
 XX The invention describes a pharmaceutical composition comprising a  
 CC polypeptide comprising an HMGB (high mobility group box) B box or its

CC functional variant to treat a disease or condition by increasing an  
 CC immune response in an individual administered with the pharmaceutical  
 CC composition. Also described are: an antibody attached to a polypeptide  
 CC comprising an HMGB B box or its functional variant; stimulating or  
 CC increasing an immune response in an individual in need of  
 CC immunostimulation; and treating cancer in an individual. The composition  
 CC is useful for stimulating or increasing an immune response in an  
 CC individual in need of immunostimulation or for treating cancer in an  
 CC individual. This is the amino acid sequence of human high mobility group  
 CC box 1 (HMGB1) B box biologically active fragment.

XX Sequence 74 AA;

Query Match 100.0%; Score 370; DB 8; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 4e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKPPSAFFLCSEYRPKIKGEHPGLSGDVAKKLGEWMNNTAADDKPYEKKAALK 60  
 DB 5 NAPKPPSAFFLCSEYRPKIKGEHPGLSGDVAKKLGEWMNNTAADDKPYEKKAALK 64  
 QY 61 EYKEDIAA 69  
 DB 65 EYKEDIAA 73

RESULT 5  
 AD071527  
 ID AD071527 standard; protein; 74 AA.

XX  
 AC AD071527;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX Human high mobility group box (HMGB) B box protein #1.  
 DE  
 XX Human; high mobility group box B box; HMGB; HMGB A box; HMGB B box;  
 KW proinflammatory cytokine; weight loss; obesity; inflammation;  
 KW inflammatory cytokine cascade; sepsis; allograft rejection;  
 KW rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;  
 KW chronic obstructive pulmonary disease; psoriasis; pancreatitis;  
 KW peritonitis; burn; myocardial ischaemia; organic ischaemia;  
 KW reperfusion ischaemia; Behcet's disease; graft-versus-host disease;  
 KW Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.

XX Homo sapiens.  
 XX  
 XX WO2004046345-A2.  
 XX  
 XX 03-JUN-2004.  
 XX  
 XX 20-NOV-2003; 2003WO-US037507.  
 XX  
 XX 20-NOV-2002; 2002US-0427841P.  
 PR 20-NOV-2002; 2002US-0427846P.  
 XX  
 XX (CRIT-) CRITICAL THERAPEUTICS INC.  
 XX  
 XX Newman W, O'keefe TL;  
 PI  
 XX WPI; 2004-420628/39.  
 DR

XX New high mobility group box proteins, useful in treating obesity, sepsis,  
 PT rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,  
 PT Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.  
 XX

XX Disclosure; SEQ ID NO 51; 113pp; English.

XX The invention relates to a polypeptide comprising a high mobility group  
 CC box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of  
 CC a proinflammatory cytokine from a cell treated with an HMGB protein. The  
 CC invention also relates to a purified preparation of antibodies that  
 CC specifically bind to the HMGB B box but do not specifically bind to non-B

CC box epitopes of HMGB, where the antibodies can inhibit release of a  
 CC proinflammatory cytokine from a cell treated with HMGB, a method for  
 CC effecting weight loss or treating obesity in a patient, a method of  
 CC determining whether a compound inhibits inflammation, a pharmaceutical  
 CC composition comprising an HMGB protein or an antibody that binds to the  
 CC protein, an agent that inhibits TNF biological activity and a method of  
 CC treating a condition in a patient characterised by activation of an  
 CC inflammatory cytokine cascade. Effecting weight loss or treating obesity  
 CC in a patient comprises administering to the patient an amount of the  
 CC polypeptide. The polypeptide, antibodies, composition and methods are  
 CC useful in treating obesity and conditions characterised by activation of  
 CC an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,  
 CC rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,  
 CC chronic obstructive pulmonary disease, psoriasis, pancreatitis,  
 CC peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion  
 CC ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,  
 CC ulcerative colitis, multiple sclerosis or cachexia. This sequence  
 CC represents a human HMGB B box polypeptide of the invention.

XX SQ Sequence 74 AA;

Query Match 100.0%; Score 370; DB 8; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 4e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPSPAFLLFCSEYRPRKIKGEHPGLSGIDVAKKLGEMWNNTAADDKQPYEKAALK 60  
 DB 5 NAPKRPSPAFLLFCSEYRPRKIKGEHPGLSGIDVAKKLGEMWNNTAADDKQPYEKAALK 64

QY 61 EYKEDIAA 69  
 DB 65 EYKEDIAA 73

RESULT 6  
 ADY85362  
 ID ADY85362 standard; protein; 74 AA.

XX AC ADY85362;  
 XX DT 02-JUN-2005 (first entry)  
 XX DE Human high mobility group box protein HMGB1 B box.

XX High mobility group box; HMGB1; immune disorder; infection;  
 KW immunosuppressive; autoimmune disease; allergy; antiallergic;  
 KW ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.;  
 KW Crohns disease; inflammation; asthma; antiasthmatic;  
 KW rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis;  
 KW antipeoriatic; systemic lupus erythematosus; dermatological; antiulcer.

XX OS Homo sapiens.  
 XX PN WO2005025604-A2.  
 XX PD 24-MAR-2005.  
 XX PF 10-SEP-2004; 2004WO-US029540.  
 XX PR 10-SEP-2003; 2003US-0502349P.  
 XX PA (GEO) GEN HOSPITAL CORP.  
 XX PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 XX PI Warren HS, Tracey KJ;  
 XX WIPI; 2005-233421/24.

XX Treating an immune pathology in an individual comprises administering an  
 PT amount of a high mobility group box (HMGB) polypeptide comprising a  
 PT vertebrate or a non-naturally occurring HMGB A or B box, or its  
 PT immunosuppressive fragment.

PS Disclosure; SEQ ID NO 37; 57pp; English.

XX The invention is based on the discovery that high mobility group box  
 CC protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when  
 CC administered with an antigen, diminishes the antibody response to the  
 CC administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B  
 CC boxes. A claimed method of treating an immune pathology in an individual  
 CC comprises administering a HMGB polypeptide comprising a vertebrate HMGB A  
 CC box, a non-naturally-occurring HMGB A box, or an immunosuppressive  
 CC fragment of the vertebrate or non-natural HMGB A box. The immune  
 CC pathology is induced by the administration of a non-human antigen, non-  
 CC self material (e.g. a cell or tissue such as bone marrow cells) or  
 CC adjuvant to the individual, by the transplantation of an organ into the  
 CC individual, or by infection from a microorganism. Claimed methods of  
 CC protecting a subject against an immune pathology, inhibiting an immune  
 CC pathology in an individual or decreasing an immune response to an  
 CC administered non-human antigen comprise administering a HMGB polypeptide  
 CC comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box,  
 CC or an immunosuppressive fragment of the vertebrate or non-natural A box.  
 CC A claimed method of treating an autoimmune disorder in an individual  
 CC comprises administering a HMGB polypeptide comprising a vertebrate HMGB A  
 CC box, a non-naturally-occurring HMGB A box, or an immunosuppressive  
 CC fragment of these, and a vertebrate or non-naturally-occurring HMGB B  
 CC box. The HMGB polypeptide is preferably a HMGB1 peptide and may be  
 CC truncated at the C-terminus. The autoimmune disease is allergy,  
 CC ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis,  
 CC psoriasis or systemic lupus erythematosus (all claimed). The present  
 CC sequence is that of the B box of human HMGB1 protein ADY85326.

XX SQ Sequence 74 AA;

Query Match 100.0%; Score 370; DB 9; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 4e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPSPAFLLFCSEYRPRKIKGEHPGLSGIDVAKKLGEMWNNTAADDKQPYEKAALK 60  
 DB 5 NAPKRPSPAFLLFCSEYRPRKIKGEHPGLSGIDVAKKLGEMWNNTAADDKQPYEKAALK 64  
 QY 61 EYKEDIAA 69  
 DB 65 EYKEDIAA 73

RESULT 7  
 ADY85078  
 ID ADY85078 standard; protein; 74 AA.

XX AC ADY85078;  
 XX DT 16-JUN-2005 (first entry)  
 XX DE Human HMGB1 A box.

XX High mobility group box; HMGB1; monoclonal antibody; antibody therapy;  
 KW sepsis; antibacterial immunosuppressive; graft rejection; arthritis;  
 KW antiarthritic; asthma; antiasthmatic; lupus erythematosus;  
 KW antiinflammatory; inflammation; dermatological;  
 KW respiratory distress syndrome; respiratory-gen.; psoriasis;  
 KW antipeoriatic; chronic obstructive pulmonary disease; pancreatitis;  
 KW peritonitis; burns; vulnery; ischemia; vasotropic; Behcets disease;  
 KW graft versus host disease; inflammatory bowel disease;  
 KW gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;  
 KW anabolic; infection; musculoskeletal disease; immune disorder.

XX OS Homo sapiens.  
 XX OS Mus sp.  
 XX OS Rattus sp.  
 XX PN WO2005026209-A2.  
 XX PD 24-MAR-2005.

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PF 10-SEP-2004; 2004WO-US029527.
XX
PR 11-SEP-2003; 2003US-0502568P.
XX
PA (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI Newman W, Qin S, Okeefe T, Obar R;
XX
DR WPI; 2005-233483/24.
XX
XX New antibody or its antigen-binding fragment specific to a vertebrate
PT high mobility group box (HMGB) A box that inhibits release of a
PT proinflammatory cytokine from a cell treated with HMGB protein, useful
PT for treating, e.g. sepsis.
XX
XX Disclosure; SEQ ID NO 2; 123pp; English.
XX
XX The invention provides antibodies, or their antigen-binding fragments,
CC that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
CC methods of detecting and/or identifying an agent that binds to an HMGB
CC polypeptide, methods of treating a condition in a subject characterized
CC by activation of an inflammatory cytokine cascade, and methods of
CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-
CC binding fragment) binds to a vertebrate HMGB A box but does not
CC specifically bind to non-A box epitopes of HMGB, and inhibits release of
CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB
CC protein. A method of treating a condition characterized by activation of
CC an inflammatory cytokine cascade comprises administering an antibody of
CC the invention, or its antigen-binding fragment. The condition is selected
CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult
CC respiratory distress syndrome, chronic obstructive pulmonary disease,
CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
CC graft versus host disease, inflammatory bowel disease, multiple sclerosis
CC and cachexia, especially sepsis, arthritis, or lupus. The present
CC sequence is that of the A box of human HMGB1 ADY85012. An identical
CC sequence is also found in rat and mouse HMGB1.
XX
XX Sequence 74 AA;
XX
Query Match 100.0%; Score 370; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 4e-38;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NAPKPPSAFFLCSEYRPKIKGEHPGLSGDVAKKLGEWMNNTAADDKQPYEKAALK 60
DB 5 NAPKPPSAFFLCSEYRPKIKGEHPGLSGDVAKKLGEWMNNTAADDKQPYEKAALK 64
QY 61 EYKEDIAA 69
DB 65 EYKEDIAA 73
RESULT 8
ID ADY85087 standard; protein; 74 AA.
XX
XX ADY85087;
AC
XX
DT 16-JUN-2005 (first entry)
XX
DE Human HMGB1 A box.
XX
XX High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
KW sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
KW antiarthritic; asthma; antiaesthetic; lupus erythematosus;
KW antiinflammatory; inflammation; dermatological;
KW respiratory distress syndrome; respiratory-gen.; psoriasis;
KW antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
KW peritonitis; burns; vulnery; ischemia; vasotropic; Behcet's disease;
KW graft versus host disease; inflammatory bowel disease;
KW gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
KW anabolic; infection; musculoskeletal disease; immune disorder.
XX

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OS Homo sapiens.
OS Mus sp.
OS Rattus sp.
XX
XX WO2005026209-A2.
XX
XX 24-MAR-2005.
XX
XX 10-SEP-2004; 2004WO-US029527.
XX
XX 11-SEP-2003; 2003US-0502568P.
XX
XX (CRIT-) CRITICAL THERAPEUTICS INC.
XX
XX Newman W, Qin S, Okeefe T, Obar R;
PI
XX
XX WPI; 2005-233483/24.
XX
XX New antibody or its antigen-binding fragment specific to a vertebrate
PT high mobility group box (HMGB) A box that inhibits release of a
PT proinflammatory cytokine from a cell treated with HMGB protein, useful
PT for treating, e.g. sepsis.
XX
XX Disclosure; SEQ ID NO 2; 123pp; English.
XX
XX The invention provides antibodies, or their antigen-binding fragments,
CC that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
CC methods of detecting and/or identifying an agent that binds to an HMGB
CC polypeptide, methods of treating a condition in a subject characterized
CC by activation of an inflammatory cytokine cascade, and methods of
CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-
CC binding fragment) binds to a vertebrate HMGB A box but does not
CC specifically bind to non-A box epitopes of HMGB, and inhibits release of
CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB
CC protein. A method of treating a condition characterized by activation of
CC an inflammatory cytokine cascade comprises administering an antibody of
CC the invention, or its antigen-binding fragment. The condition is selected
CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult
CC respiratory distress syndrome, chronic obstructive pulmonary disease,
CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
CC graft versus host disease, inflammatory bowel disease, multiple sclerosis
CC and cachexia, especially sepsis, arthritis, or lupus. The present
CC sequence is that of the A box of human HMGB1 ADY85012. An identical
CC sequence is also found in rat and mouse HMGB1.
XX
XX Sequence 74 AA;
XX
Query Match 100.0%; Score 370; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 4e-38;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NAPKPPSAFFLCSEYRPKIKGEHPGLSGDVAKKLGEWMNNTAADDKQPYEKAALK 60
DB 5 NAPKPPSAFFLCSEYRPKIKGEHPGLSGDVAKKLGEWMNNTAADDKQPYEKAALK 64
QY 61 EYKEDIAA 69
DB 65 EYKEDIAA 73
RESULT 9
ID ADR45941 standard; protein; 75 AA.
XX
XX ADR45941;
AC
XX
XX 21-OCT-2004 (first entry)
DT
XX
XX Human high mobility group HMGB1 HMG-BOX(large) protein.
DE
XX
XX antidiabetic; ophthalmological; nephropathic; antiarthritic;
KW antiinflammatory; cytostatic; gynaecological; antipsoriatic;
KW dermatological; antiviral; vasotropic; antiarteriosclerotic; antianginal;
KW

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KW cardiant; vulnery; antiulcer; high mobility group protein; human.  
 XX Homo sapiens.  
 OS WO2004061456-A2.  
 PN 22-JUL-2004.  
 PD 05-JAN-2004; 2004WO-EP000030.  
 PF 03-JAN-2003; 2003DE-01000023.  
 PR 07-MAR-2003; 2003DE-01010160.  
 PR 10-AUG-2003; 2003DE-01036642.  
 PR 08-OCT-2003; 2003DE-01046614.  
 XX (ALCE-) ALCEDO BIOTECH GMBH.  
 PA Bullerdiel J;  
 XX WPI; 2004-571355/55.  
 PI N-PSDB; ADR45975.  
 DR Use of nucleic acids encoding basic DNA-binding proteins, and their  
 XX translation or transcription products, for treating diseases associated  
 PT with e.g. angiogenesis, neovascularization or wound healing, also for  
 PT drug screening.  
 PT Claim 57; SEQ ID NO 26; 161pp; German.  
 PS The present invention relates to the use, especially in vitro, of nucleic  
 XX acids encoding high mobility group proteins for the following processes:  
 CC angiogenesis (including in a wound bed), neovascularization,  
 CC transmyocardial revascularization, wound healing, epithelialization and  
 CC healing in cases of tooth or bone implants. The sequences and their  
 CC encoded protein are useful for treating a very wide range of diseases:  
 CC (proliferative) diabetic retinopathy, diabetic nephropathy, macular  
 CC degeneration, arthritis, endometriosis, histiocytosis, psoriasis,  
 CC rosacea, eruptive or cavernous haemangioma, tumours (especially melanoma,  
 CC Kaposi sarcoma and basal cell carcinoma), haemorrhoids, arteriosclerosis,  
 CC angina pectoris, ischaemia, infarction, infertility, wounds (including  
 CC diabetic and other ulcers), also diseases associated with DNA damage,  
 CC especially xeroderma pigmentosum, 'leather skin', skin cancers and ageing  
 CC (including where associated with sunburn) and cardiac infarct, including  
 CC cosmetic treatment, especially as a sun-protection composition. Compounds  
 CC identified as modulators of the specified processes can also be used  
 CC therapeutically. The present sequence is a polypeptide of the invention.  
 XX  
 SQ Sequence 75 AA;  
 Query Match 100.0%; Score 370; DB 8; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSLGIDVAKLGEWNNNTAADDKQPYEKKAAKLK 60  
 DB 2 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSLGIDVAKLGEWNNNTAADDKQPYEKKAAKLK 61  
 QY 61 EKYKDIAA 69  
 DB 62 EKYKDIAA 70  
 RESULT 10  
 AD025962  
 ID AD025962 standard; peptide; 92 AA.  
 XX  
 AC AD025962;  
 XX  
 XX 26-AUG-2004 (first entry)  
 DT  
 XX High mobility group box 1 B box fragment seqid 45.  
 DE  
 XX cytostatic; gene therapy; vaccine; pharmaceutical composition;  
 KW

KW HMGB B box; high mobility group; immune response; immunostimulation;  
 KW cancer; human; high mobility group box 1; HMGI; cytokine activity; B box.  
 OS Homo sapiens.  
 XX WO2004046338-A2.  
 PN 03-JUN-2004.  
 PD 19-NOV-2003; 2003WO-US036975.  
 PF 20-NOV-2002; 2002US-0427848P.  
 PR (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 PA Tracey KJ;  
 XX WPI; 2004-420625/39.  
 PI New pharmaceutical composition comprises a polypeptide comprising an HMGB  
 XX B box or its functional variant; useful for stimulating or increasing an  
 PT immune response in an individual or for treating cancer in an individual.  
 PT Disclosure; SEQ ID NO 45; 68pp; English.  
 XX The invention describes a pharmaceutical composition comprising a  
 PS polypeptide comprising an HMGB (high mobility group box) B box or its  
 XX functional variant to treat a disease or condition by increasing an  
 CC immune response in an individual administered with the pharmaceutical  
 CC composition. Also described are: an antibody attached to a polypeptide  
 CC comprising an HMGB B box or its functional variant; stimulating or  
 CC increasing an immune response in an individual in need of  
 CC immunostimulation; and treating cancer in an individual. The composition  
 CC is useful for stimulating or increasing an immune response in an  
 CC individual in need of immunostimulation or for treating cancer in an  
 CC individual. This is the amino acid sequence of human high mobility group  
 CC box 1 (HMGI) B box biologically active fragment.  
 XX  
 SQ Sequence 92 AA;  
 Query Match 100.0%; Score 370; DB 8; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSLGIDVAKLGEWNNNTAADDKQPYEKKAAKLK 60  
 DB 5 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSLGIDVAKLGEWNNNTAADDKQPYEKKAAKLK 64  
 QY 61 EKYKDIAA 69  
 DB 65 EKYKDIAA 73  
 RESULT 11  
 AD071534  
 ID AD071534 standard; protein; 92 AA.  
 XX  
 AC AD071534;  
 XX  
 XX 26-AUG-2004 (first entry)  
 DT  
 XX Human high mobility group box (HMGB) B box protein #7.  
 DE  
 XX Human; high mobility group box B box; HMGB; HMGB A box; HMGB B box;  
 KW proinflammatory cytokine; weight loss; obesity; inflammation;  
 KW inflammatory cytokine cascade; sepsis; allograft rejection;  
 KW rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;  
 KW chronic obstructive pulmonary disease; psoriasis; pancreatitis;  
 KW peritonitis; burn; myocardial ischaemia; organic ischaemia;  
 KW reperfusion ischaemia; Behcet's disease; graft-versus-host disease;  
 KW Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.  
 XX  
 OS Homo sapiens.



XX W02004046345-A2.  
 XX 03-JUN-2004.  
 XX 20-NOV-2003; 2003WO-US037507.  
 XX 20-NOV-2002; 2002US-0427841P.  
 XX 20-NOV-2002; 2002US-0427846P.  
 XX (CRIT-) CRITICAL THERAPEUTICS INC.  
 XX Newman W, O'keefe TL;  
 XX WFI; 2004-420628/39.  
 XX New high mobility group box proteins, useful in treating obesity, sepsis,  
 XX rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,  
 XX Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.  
 XX Disclosure; SEQ ID NO 58; 113pp; English.  
 XX  
 CC The invention relates to a polypeptide comprising a high mobility group  
 CC box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of  
 CC a proinflammatory cytokine from a cell treated with an HMGB protein. The  
 CC invention also relates to a purified preparation of antibodies that  
 CC specifically bind to the HMGB B box but do not specifically bind to non-B  
 CC box epitopes of HMGB, where the antibodies can inhibit release of a  
 CC proinflammatory cytokine from a cell treated with HMGB, a method for  
 CC effecting weight loss or treating obesity in a patient, a method of  
 CC determining whether a compound inhibits inflammation, a pharmaceutical  
 CC composition comprising an HMGB protein or an antibody that binds to the  
 CC protein, an agent that inhibits TNF biological activity and a method of  
 CC treating a condition in a patient characterised by activation of an  
 CC inflammatory cytokine cascade. Effecting weight loss or treating obesity  
 CC in a patient comprises administering to the patient an amount of the  
 CC polypeptide. The polypeptide, antibodies, composition and methods are  
 CC useful in treating obesity and conditions characterised by activation of  
 CC an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,  
 CC rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,  
 CC chronic obstructive pulmonary disease, psoriasis, pancreatitis,  
 CC peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion  
 CC ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,  
 CC ulcerative colitis, multiple sclerosis or cachexia. This sequence  
 CC represents a human HMGB B box polypeptide of the invention.  
 XX  
 SQ Sequence 92 AA;  
 Query Match 100.0%; Score 370; DB 8; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NAPRRPPSAFFLCSEYRPKIKGEHPGLSGIDVAKKLGMWNNNTAADKQPYEKAALK 60  
 DB |||||||||  
 5 NAPRRPPSAFFLCSEYRPKIKGEHPGLSGIDVAKKLGMWNNNTAADKQPYEKAALK 64  
 QY 61 EYKEKDIAA 69  
 DB |||||||||  
 65 EYKEKDIAA 73  
 RESULT 12  
 ADY85368  
 ID ADY85368 standard; protein; 92 AA.  
 XX  
 AC ADY85368;  
 XX 02-JUN-2005 (first entry)  
 XX Human high mobility group box protein HMGB1 B box.  
 XX High mobility group box; HMGB1; immune disorder; infection;  
 XX immunosuppressive; autoimmune disease; allergy; anti-allergic;  
 KW

KW ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.;  
 KW Crohn's disease; inflammation; asthma; antiasthmatic;  
 KW rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis;  
 KW antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.  
 XX Homo sapiens.  
 XX W02005025604-A2.  
 XX 24-MAR-2005.  
 XX 10-SEP-2004; 2004WO-US029540.  
 XX 10-SEP-2003; 2003US-0502349P.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 XX Warren HS, Tracey KJ;  
 XX WFI; 2005-233421/24.  
 XX  
 PT Treating an immune pathology in an individual comprises administering an  
 PT amount of a high mobility group box (HMGB) polypeptide comprising a  
 PT vertebrate or a non-naturally occurring HMGB A or B box, or its  
 PT immunosuppressive fragment.  
 XX  
 PS Disclosure; SEQ ID NO 43; 57pp; English.  
 XX  
 CC The invention is based on the discovery that high mobility group box  
 CC protein 1 (HMGB1, also known as high mobility group-1 or HMGB1), when  
 CC administered with an antigen, diminishes the antibody response to the  
 CC administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B  
 CC boxes. A claimed method of treating an immune pathology in an individual  
 CC comprises administering a HMGB polypeptide comprising a vertebrate HMGB A  
 CC box, a non-naturally-occurring HMGB A box, or an immunosuppressive  
 CC fragment of the vertebrate or non-natural HMGB A box. The immune  
 CC pathology is induced by the administration of a non-human antigen, non-  
 CC self material (e.g. a cell or tissue such as bone marrow cells) or  
 CC adjuvant to the individual, by the transplantation of an organ into the  
 CC individual, or by infection from a microorganism. Claimed methods of  
 CC protecting a subject against an immune pathology, inhibiting an immune  
 CC pathology in an individual or decreasing an immune response to an  
 CC administered non-human antigen comprise administering a HMGB polypeptide  
 CC comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box,  
 CC or an immunosuppressive fragment of the vertebrate or non-natural A box.  
 CC A claimed method of treating an autoimmune disorder in an individual  
 CC comprises administering a HMGB polypeptide comprising a vertebrate HMGB A  
 CC box, a non-naturally-occurring HMGB A box, or an immunosuppressive  
 CC fragment of these, and a vertebrate or non-naturally-occurring HMGB B  
 CC box. The HMGB polypeptide is preferably a HMGB1 peptide and may be  
 CC truncated at the C-terminus. The autoimmune disease is allergy,  
 CC ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis,  
 CC psoriasis or systemic lupus erythematosus (all claimed). The present  
 CC sequence is that of the B box of human HMGB1 protein.  
 XX  
 SQ Sequence 92 AA;  
 Query Match 100.0%; Score 370; DB 9; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NAPRRPPSAFFLCSEYRPKIKGEHPGLSGIDVAKKLGMWNNNTAADKQPYEKAALK 60  
 DB |||||||||  
 5 NAPRRPPSAFFLCSEYRPKIKGEHPGLSGIDVAKKLGMWNNNTAADKQPYEKAALK 64  
 QY 61 EYKEKDIAA 69  
 DB |||||||||  
 65 EYKEKDIAA 73  
 RESULT 13  
 ADY85084

ID ADY85084 standard; protein; 92 AA.  
 AC ADY85084;  
 DT 16-JUN-2005 (first entry)  
 XX Human HMGB1 A box.  
 DE  
 XX High mobility group box; HMGB1; monoclonal antibody; antibody therapy;  
 KW sepsis; antibacterial immunosuppressive; graft rejection; arthritis;  
 KW antiarthritic; asthma; antiasthmatic; lupus erythematosus;  
 KW antiinflammatory; inflammation; dermatological;  
 KW respiratory distress syndrome; respiratory-gen.; psoriasis;  
 KW antipariatic; chronic obstructive pulmonary disease; pancreatitis;  
 KW peritonitis; burns; vulnary; ischemia; vasotropic; Behcets disease;  
 KW graft versus host disease; inflammatory bowel disease;  
 KW gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;  
 KW anabolic; infection; musculoskeletal disease; immune disorder.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Rattus sp.  
 XX  
 PN WO2005026209-A2.  
 XX  
 PN 24-MAR-2005.  
 XX  
 PD 10-SEP-2004; 2004WO-US029527.  
 XX  
 PF 11-SEP-2003; 2003US-0502568P.  
 XX  
 PR (CRIT-) CRITICAL THERAPEUTICS INC.  
 XX  
 PA Newman W, Qin S, Okeefe T, Obar R;  
 PI WPI; 2005-233483/24.  
 XX  
 XX New antibody or its antigen-binding fragment specific to a vertebrate  
 PT high mobility group box (HMGB) A box that inhibits release of a  
 PT proinflammatory cytokine from a cell treated with HMGB protein, useful  
 PT for treating, e.g. sepsis.  
 XX  
 PS Disclosure; SEQ ID NO 2; 123pp; English.  
 XX  
 CC The invention provides antibodies, or their antigen-binding fragments,  
 CC that bind to a vertebrate high mobility group box (HMGB) polypeptide, to  
 CC methods of detecting and/or identifying an agent that binds to an HMGB  
 CC polypeptide, methods of treating a condition in a subject characterized  
 CC by activation of an inflammatory cytokine cascade, and methods of  
 CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-  
 CC binding fragment) binds to a vertebrate HMGB A box but does not  
 CC specifically bind to non-A box epitopes of HMGB, and inhibits release of  
 CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB  
 CC protein. A method of treating a condition characterized by activation of  
 CC an inflammatory cytokine cascade comprises administering an antibody of  
 CC the invention, or its antigen-binding fragment. The condition is selected  
 CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult  
 CC respiratory distress syndrome, chronic obstructive pulmonary disease,  
 CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,  
 CC graft versus host disease, inflammatory bowel disease, multiple sclerosis  
 CC and cachexia, especially sepsis, arthritis, or lupus. The present  
 CC sequence is that of the A box of human HMGB1 ADY85012. An identical  
 CC sequence is also found in rat and mouse HMGB1.  
 XX  
 SQ Sequence 92 AA;  
 Query Match 100.0%; Score 370; DB 9; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NAPKRPSPAFFLFCSEYRPRKIKGEHPGLSGIDVAKLGEWMNNTAADDKQPYEKKAAKLK 60  
 DB 5 NAPKRPSPAFFLFCSEYRPRKIKGEHPGLSGIDVAKLGEWMNNTAADDKQPYEKKAAKLK 64

QY 61 EYKEDIAA 69  
 DB 65 EYKEDIAA 73  
 RESULT 14  
 AAB57179  
 ID AAB57179 standard; protein; 128 AA.  
 XX  
 AC AAB57179;  
 XX  
 DT 13-MAR-2001 (first entry)  
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1757.  
 XX  
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;  
 KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
 KW wound; infectious disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055174-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US005988.  
 XX  
 PR 12-MAR-1999; 99US-0124270P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (ROSE/) ROSEN C A.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-587513/55.  
 DR N-PSDB; AAF16382.  
 XX  
 PT Prostate cancer associated gene sequences, referred to as prostate cancer  
 PT antigens, useful for treatment, prevention, and diagnosis of disorders  
 PT such as prostate cancer.  
 XX  
 PS Claim 11; Page 2225-2226; 2338pp; English.  
 XX  
 CC AAF15566 to AAF16505 encode the human prostate cancer associated  
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
 CC The prostate cancer antigens can have neuroprotective, cytostatic,  
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
 CC and can be used in gene therapy. The prostate cancer antigen  
 CC polynucleotides may be used for detection of prostate cancer, chromosome  
 CC identification, as chromosome markers, and for numerous other diagnostic  
 CC or research purposes. The prostate cancer antigens may be used to treat  
 CC disorders such as neural, immune, muscular, reproductive,  
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to  
 CC AAB57303 represent sequences used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 128 AA;  
 Query Match 100.0%; Score 370; DB 3; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-38;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NAPKRPSPAFFLFCSEYRPRKIKGEHPGLSGIDVAKLGEWMNNTAADDKQPYEKKAAKLK 60  
 DB 10 NAPKRPSPAFFLFCSEYRPRKIKGEHPGLSGIDVAKLGEWMNNTAADDKQPYEKKAAKLK 69  
 QY 61 EYKEDIAA 69

Db 70 EYKEDIAA 78  
 |||||  
 1 NAKRPSPAFLLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKOPYEKKAAKLK 60  
 61 NAKRPSPAFLLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKOPYEKKAAKLK 120  
 Qy 61 EYKEDIAA 69  
 |||||  
 Db 121 EYKEDIAA 129  
 Search completed: April 6, 2006, 10:19:12  
 Job time : 83.7533 secs

RESULT 15  
 ABM81641  
 ID ABM81641 standard; protein; 168 AA.  
 XX ABM81641;  
 AC  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Tumour-associated antigenic target (TAT) polypeptide PRO82460, SEQ:4238.  
 XX  
 KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;  
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
 KW central nervous system cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;  
 KW chromosome identification; chromosome mapping; gene mapping;  
 KW gene therapy; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004030615-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 29-SEP-2003; 2003WO-US028547.  
 XX  
 PR 02-OCT-2002; 2002US-0414971P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Wu TD, Zhang Z, Zhou Y;  
 XX  
 DR WPI; 2004-347921/32.  
 DR N-PSDB; ACN39840.  
 XX  
 PT New tumor-associated antigenic target polypeptides and nucleic acids,  
 PT useful in preparing a medicament for treating or detecting a  
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
 PT prostate cancer or tumor.  
 XX  
 PS Claim 12; SEQ ID NO 4238; 7273pp; English.  
 XX  
 CC The invention relates to human tumour-associated antigenic target (TAT)  
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are  
 CC overexpressed in cancer tissues compared to normal tissues, and may thus  
 CC serve as effective targets for the diagnosis and treatment of cancer in  
 CC mammals. The invention also relates to nucleic acid and polypeptide  
 CC sequences at least 80% identical to the TAT nucleic acids and  
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic  
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic  
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a  
 CC TAT polypeptide; and methods and compositions for the treatment or  
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
 CC antibodies, antagonists, binding molecules and compositions are useful  
 CC for diagnosing or treating a cell proliferative disorder associated with  
 CC increased TAT expression, particularly cancers such as breast cancer,  
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
 CC used as hybridisation probes, in chromosome and gene mapping, in  
 CC chromosome identification and in gene therapy. The present sequence  
 CC represents a TAT polypeptide of the invention  
 XX  
 SQ Sequence 168 AA;  
 Query Match 100.0%; Score 370; DB 8; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 1e-37;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:19:38 ; Search time 13.1645 Seconds  
(without alignments)  
504.309 Million cell updates/sec

Title: US-10-717-984-5

Perfect score: 370

Sequence: 1 NAPKRPPSAFFLFCSEYRPK.....QPYEKKAALKKEKYKDIAA 69

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80.\*

2: PIR1.\*

3: PIR2.\*

4: PIR3.\*

5: PIR4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	170	2	NSRTH1
2	370	100.0	215	1	nonhistone chromos
3	370	100.0	215	1	nonhistone chromos
4	370	100.0	215	2	nonhistone chromos
5	370	100.0	215	2	non-histone chromo
6	365	98.6	215	2	nonhistone chromos
7	360	97.3	216	2	nonhistone chromos
8	335	90.5	210	2	high mobility grou
9	324	87.6	186	2	nonhistone chromos
10	324	87.6	209	1	nonhistone chromos
11	324	87.6	210	2	nonhistone chromos
12	321	86.8	207	2	nonhistone chromos
13	319	86.2	207	2	high-mobility grou
14	316	85.4	210	2	high mobility grou
15	301	81.4	172	2	nonhistone chromos
16	301	81.4	204	2	high-mobility-grou
17	300	81.1	201	2	HMG-1 - chicken
18	300	80.1	202	2	nonhistone chromos
19	298	80.5	204	2	high mobility grou
20	294	79.5	205	2	nonhistone chromos
21	292	78.9	186	2	nonhistone chromos
22	263	71.1	215	2	gene HMG-T2 protei
23	172	46.5	708	2	DNA-binding protei
24	170	45.9	709	2	structure-specific
25	168.5	45.5	138	2	high mobility grou
26	168	45.4	669	2	high mobility grou
27	166	44.9	200	2	HMG1 protein - sea
28	166	44.9	393	2	dorsal switch prot
29	166	44.9	393	2	nonhistone chromos

30	164.5	44.5	141	2	T09581	probable high mobi
31	164	44.3	561	2	S35637	high mobility grou
32	163	44.1	93	2	A35072	nonhistone chromos
33	162.5	43.9	149	2	S39556	high mobility grou
34	160.5	43.4	139	2	T03372	high mobility grou
35	159.5	43.1	141	2	T07377	high mobility grou
36	159	43.0	642	2	T12113	transcription fact
37	158.5	42.8	157	2	B47150	high mobility grou
38	158.5	42.8	161	2	S18991	high mobility grou
39	158.5	42.8	168	2	T03640	high mobility grou
40	157.5	42.6	142	2	T02252	high mobility grou
41	157.5	42.6	144	2	S40302	high mobility grou
42	156.5	42.3	178	2	T51159	HMG protein (impor
43	156	42.2	99	2	S78076	nonhistone chromos
44	155.5	42.0	126	2	T03375	high mobility grou
45	152.5	41.2	141	2	T51598	high mobility grou

#### ALIGNMENTS

##### RESULT 1

A27853 nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)

C:Species: Cricetus griseus (Chinese hamster)

C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004

C:Accession: A27853

Nucleic Acids Res. 15, 5051-5068, 1987

R:Lee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.

A:Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA s

A:Reference number: A27853; MUID:87259986; PMID:3601666

A:Accession: A27853

A:Molecule type: mRNA

A:Residues: 1-170 <LEE>

A:Cross-references: UNIPROT:P07156; UNIPARC:UPI00001771D5

C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology

C:Keywords: chromosomal protein; DNA binding; nucleus

F:1-38/Domain: HMG box homology (fragment) <HMG1>

F:47-121/Domain: HMG box homology <HMG2>

Query Match 100.0%; Score 370; DB 2; Length 170;

Best Local Similarity 100.0%; Pred. No. 3.8e-33;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSGDVAKKLGEWMNNTAADDKQYEKKAALK 60

DB 48 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSGDVAKKLGEWMNNTAADDKQYEKKAALK 107

QY 61 EYKEDIAA 69

DB 108 EYKEDIAA 116

##### RESULT 2

NSRTH1

nonhistone chromosomal protein HMG-1 - rat

N:Alternate names: 30K heparin-binding protein, brain; amphoterin

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004

C:Accession: A41175; A27298; A30188; B48771; A48771; C48771

R:Meremisa, J.; Pihlaskari, R.; Laitinen, J.; Wartiovaara, J.; Rauvala, H.

J. Biol. Chem. 266, 16722-16729, 1991

A:Title: 30-KDa heparin-binding protein of brain (amphoterin) involved in neurite outgro

A:Reference number: A41175; MUID:91358468; PMID:1885601

A:Accession: A41175

A:Molecule type: mRNA

A:Residues: 1-215 <MER>

A:Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; GB:M64986; NID:G202884; PTDN:

A:Note: part of this sequence, including the amino end of the mature protein, was confir

A:Note: the authors used antibodies to synthetic peptides to demonstrate this protein in

h-mobility group proteins

R:Paonessa, G.; Frank, R.; Cortese, R.

Nucleic Acids Res. 15, 9077, 1987

A;Title: Nucleotide sequence of rat liver HMG1 cDNA.  
A;Reference number: A27298; MUID:88067717; PMID:3684582  
A;Accession: A27298  
A;Molecule type: mRNA  
A;Residues: 1-10,'R',12-82,84-95,97,'AS',100-215 <PAO>  
A;Cross-references: UNIPARC:UPI0000173984  
R;Rauvala, H.; Meremies, J.; Pihlaskari, R.; Korkolainen, M.; Huhtala, M.L.; Panula, P.  
J. Cell Biol. 107, 2293-2305, 1998  
A;Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal  
brain neurons.  
A;Reference number: A30188; MUID:89068894; PMID:2461949  
A;Accession: A30188  
A;Molecule type: protein  
A;Residues: 2-14,'X',16-21 <RAU>  
A;Cross-references: UNIPARC:UPI0000173985  
R;Parkkinen, J.; Raulo, E.; Meremies, J.; Nolo, R.; Kajander, E.O.; Baumann, M.; Rauvala  
J. Biol. Chem. 268, 19726-19738, 1993  
A;Title: Amphoterin, the 30-kDa protein in a family of HMG1-type polypeptides. Enhanced  
A;Reference number: A48771; MUID:93374971; PMID:8366113  
A;Accession: B48771  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 98-105,'X',107-112 <PA2>  
A;Cross-references: UNIPARC:UPI0000173986  
A;Experimental source: postnatal brain  
A;Note: sequence extracted from NCBI backbone (NCBIP:137788)  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein; DNA binding; nucleus  
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status experimental <WAT>  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 100.0%; Score 370; DB 1; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.9e-33;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60  
|||||  
Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 152  
|||||  
Qy 61 EYKEDIAA 69  
|||||  
Db 153 EYKEDIAA 161  
|||||

RESULT 3  
S01947  
nonhistone chromosomal protein HMG-1 - bovine  
N;Alternate names: 33K protein; high-mobility-group protein HMG-1  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 30-Sep-1989 #sequence revision 22-Apr-1995 #text\_change 09-Jul-2004  
C;Accession: S01947; A61611; S10959; I45910  
R;Kaplan, D.J.; Duncan, C.H.  
Nucleic Acids Res. 16, 10375, 1988  
A;Title: Full length cDNA sequence for bovine high mobility group 1 (HMG1) protein.  
A;Reference number: S01947; MUID:89057489; PMID:3194213  
A;Accession: S01947  
A;Molecule type: mRNA  
A;Residues: 1-215 <KAP>  
A;Cross-references: UNIPROT:P10103; UNIPARC:UPI000016C31D; EMBL:X12796; PIDN:C  
R;Walker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.  
FEBS Lett. 122, 264-270, 1980  
A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.  
A;Reference number: A61611; MUID:81138848; PMID:7202717  
A;Accession: A61611  
A;Molecule type: protein  
A;Residues: 2-22,'S',24-40,48-105,'A',107-157,'X',160-193,'D',195 <WAL>  
A;Cross-references: UNIPARC:UPI0000173987; UNIPARC:UPI0000173988  
R;Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.  
FEBS Lett. 267, 139-141, 1990  
A;Title: High mobility group proteins 1 and 2 bind preferentially to brominated poly(dG-  
A;Reference number: S10726; MUID:90306387; PMID:2365081  
A;Accession: S10959

A;Molecule type: protein  
A;Residues: 2-22,'X',24-38 <CHR>  
A;Cross-references: UNIPARC:UPI0000173989  
R;Pentecost, B.T.; Dixon, G.H.  
Biosci. Rep. 4, 49-57, 1984  
A;Title: Isolation and partial sequence of bovine cDNA clones for the high-mobility-group  
A;Reference number: I45910; MUID:84128872; PMID:6141822  
A;Accession: I45910  
A;Status: preliminary; translated from GB/EMBL/DBDJB  
A;Molecule type: mRNA  
A;Residues: 'GGG',119,'V',121-215 <PEN>  
A;Cross-references: UNIPARC:UPI000016C31E; GB:M26110; NID:G163156; PIDN:AAA30567.1; PID:G  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein; DNA binding; duplication; nucleus  
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status predicted <WAT>  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 100.0%; Score 370; DB 1; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.9e-33;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60  
|||||  
Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 152  
|||||  
Qy 61 EYKEDIAA 69  
|||||  
Db 153 EYKEDIAA 161  
|||||

RESULT 4  
S02826  
nonhistone chromosomal protein HMG-1 - human  
C;Species: Homo sapiens (man)  
C;Date: 01-Dec-1989 #sequence revision 01-Dec-1989 #text\_change 09-Jul-2004  
C;Accession: S02826; A33178; G33178  
R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.  
Nucleic Acids Res. 17, 1197-1214, 1989  
A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.  
A;Reference number: S02826; MUID:89160247; PMID:2922262  
A;Accession: S02826  
A;Molecule type: mRNA  
A;Residues: 1-215 <WEN>  
A;Cross-references: UNIPROT:P09429; UNIPARC:UPI0000015ED; EMBL:X12597; NID:G32326; PIDN  
R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.  
Electrophoresis 11, 883-891, 1990  
A;Title: Development of a database of amino acid sequences for human colon carcinoma prot  
A;Reference number: A33178; MUID:91176935; PMID:2079031  
A;Accession: A33178  
A;Molecule type: protein  
A;Residues: 2-13,'XXF', <WAR>  
A;Cross-references: UNIPARC:UPI00001771D7  
A;Accession: G33178  
A;Molecule type: protein  
A;Residues: 2-13,'XX',16-22 <WA2>  
A;Cross-references: UNIPARC:UPI00001771D7  
C;Genetics:

A;Gene: GDB:HMGI  
A;Cross-references: GDB:133789; OMIM:163905  
A;Map position: 13q12-13q12  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein; DNA binding; nucleus  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>  
  
Query Match 100.0%; Score 370; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.9e-33;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60  
|||||  
Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 152  
|||||

C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C:Keywords: chromosomal protein; DNA binding; nucleus  
F:6-83/Domain: HMG box homology <HMGI>  
F:92-166/Domain: HMG box homology <HMG2>

Query Match 98.6%; Score 365; DB 2; Length 215;  
Best Local Similarity 98.6%; Pred. No. 1.7e-32;  
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEWMNNTAADDKQPYEKKAALK 60  
Db 93 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEWMNNTAADDKQPYEKKAALK 152

Qy 61 EYKEDIAA 69  
Db 153 EYKEDIAA 161

RESULT 7  
S29857  
nonhistone chromosomal protein HMG-1 - human  
C:Species: Homo sapiens (man)  
C:Date: 08-Dec-1993 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S29857  
F:Stros, M.; Dixon, G.H.  
Biochim. Biophys. Acta 1172, 231-235, 1993  
A:Title: A retropseudogene for non-histone chromosomal protein HMG-1.  
A:Reference number: S29857; MUID:93176821; PMID:84395568  
A:Accession: S29857  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-216 <STR>  
A:Cross-references: UNIPARC:UPI000011DFAA; EMBL:L08048; NID:g184250; PIDN:AAA64970.1; PI  
A:Note: the authors did not translate the codon for residue 1  
C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C:Keywords: chromosomal protein  
F:6-83/Domain: HMG box homology <HMGI>  
F:92-166/Domain: HMG box homology <HMG2>

Query Match 97.3%; Score 360; DB 2; Length 216;  
Best Local Similarity 98.6%; Pred. No. 6.1e-32;  
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEWMNNTAADDKQPYEKKAALK 60  
Db 93 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEWMNNTAADDKQPYEKKAALK 152

Qy 61 EYKEDIAA 69  
Db 153 EYKEDIAA 161

RESULT 8  
S62355  
high mobility group protein 1 - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S62355  
F:Nightingale, K.; Dimitrov, S.; Reeves, R.; Wolffe, A.P.  
EMBO J. 15, 548-561, 1996  
A:Title: Evidence for a shared structural role for HMGI and linker histones B4 and H1 in  
A:Reference number: S62355; MUID:96174815; PMID:8599938  
A:Accession: S62355  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-210 <NIG>  
A:Cross-references: UNIPROT:Q91596; UNIPARC:UPI00000FB3E3; EMBL:U21933; NID:g709958; PID  
A:Note: the authors did not translate the codon for residue 1  
C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
F:6-82/Domain: HMG box homology <HMG1>  
F:91-165/Domain: HMG box homology <HMG2>

Query Match 90.5%; Score 335; DB 2; Length 210;





Best Local Similarity 85.5%; Pred. No. 1.1e-27;  
Matches 59; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 NAKRPPSAFLFCSEYRPKIKGEHPGLSGDVAKKLGENMWNNTAADDKQPYEKKAAKLK 60  
|||||  
Db 93 NAKRPPSAFLFCSEYRPKIKNDHPGLSGDTAKKLGENMWSQSAKDKQPYEQKAAKLK 152  
|||||  
Qy 61 EYKEDIAA 69  
|||||  
Db 153 EYKEDIAA 161

## RESULT 13

JC1114  
high-mobility group protein 2 - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 09-Jul-2004  
C;Accession: JC1114  
R;Davis, D.L.; Burch, J.B.E.  
Gene 113, 251-256, 1992  
A;Title: Isolation of a chicken HMG2 cDNA clone and evidence for an HMG2-specific 3'-untranslated region  
A;Reference number: JC1114; MUID:92241676; PMID:1572546  
A;Accession: JC1114  
A;Molecule type: mRNA  
A;Residues: 1-207 <DAV>  
A;Cross-references: UNIPROT:P26584; UNIPARC:UPI0000171347; GB:M83235; NID:9211926; PIDN:1114  
C;Comment: The high mobility group proteins are among the most abundant nonhistone chromosomal proteins  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: DNA binding; nucleus  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 86.2%; Score 319; DB 2; Length 207;  
Best Local Similarity 85.5%; Pred. No. 1.8e-27;  
Matches 59; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 NAKRPPSAFLFCSEYRPKIKGEHPGLSGDVAKKLGENMWNNTAADDKQPYEKKAAKLK 60  
|||||  
Db 93 NAKRPPSAFLFCSEYRPKIKNDHPGLSGDTAKKLGENMWSQSAKDKQPYEQKAAKLK 152  
|||||  
Qy 61 EYKEDIAA 69  
|||||  
Db 153 EYKEDIAA 161

## RESULT 14

S54774  
high mobility group 2 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S54774; S52211  
R;Zwilling, S.; Koenig, H.; Wirth, T.  
EMBO J. 14, 1198-1208, 1995  
A;Title: High mobility group protein 2 functionally interacts with the POU domains of oocyte transcription factors  
A;Reference number: S54774; MUID:95237201; PMID:7720710  
A;Accession: S54774  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-210 <ZWI>  
A;Cross-references: UNIPROT:P30681; UNIPARC:UPI000016432C; EMBL:Z46757; NID:9609168; PIDN:1114  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 85.4%; Score 316; DB 2; Length 210;  
Best Local Similarity 87.0%; Pred. No. 3.8e-27;  
Matches 60; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 NAKRPPSAFLFCSEYRPKIKGEHPGLSGDVAKKLGENMWNNTAADDKQPYEKKAAKLK 60  
|||||  
Db 93 NAKRPPSAFLFCSEYRPKIKNDHPGLSGDTAKKLGENMWSQSAKDKQPYEQKAAKLK 152  
|||||  
Qy 61 EYKEDIAA 69

Db 153 EYKEDIAA 161  
|||||

## RESULT 15

A24019  
nonhistone chromosomal protein HMG-T - trout (fragment)  
N;Alternate names: HMG-T  
C;Species: Salmo gairdneri (trout)  
C;Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 09-Jul-2004  
C;Accession: A24019  
R;Pentecost, B.T.; Wright, J.M.; Dixon, G.H.  
Nucleic Acids Res. 13, 4871-4888, 1985  
A;Title: Isolation and sequence of cDNA clones coding for a member of the family of high-mobility group proteins  
A;Reference number: A24019; MUID:85269614; PMID:4022777  
A;Accession: A24019  
A;Molecule type: mRNA  
A;Residues: 1-172 <PEN>  
A;Cross-references: UNIPROT:P07746; UNIPARC:UPI00001771D6  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein; DNA binding; nucleus  
F;1-50/Domain: HMG box homology (fragment) <HMG1>  
F;59-133/Domain: HMG box homology <HMG2>

Query Match 81.4%; Score 301; DB 2; Length 172;  
Best Local Similarity 78.3%; Pred. No. 1.3e-25;  
Matches 54; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 NAKRPPSAFLFCSEYRPKIKGEHPGLSGDVAKKLGENMWNNTAADDKQPYEKKAAKLK 60  
|||||  
Db 60 NAKRPPSAFLFCSEYRPKIKNDHPGLSGDTAKKLGENMWSQSAKDKQPYEQKAAKLK 119  
|||||

Qy 61 EYKEDIAA 69  
|||||

Db 120 EYKEDITA 128

Search completed: April 6, 2006, 10:26:19  
Job time : 14.1645 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.  
OM protein - protein search, using sw model  
Run on: April 6, 2006, 10:13:48 ; Search time 81.4836 Seconds  
(without alignments)  
597.439 Million cell updates/sec

Title: US-10-717-984-5  
Perfect score: 370  
Sequence: 1 NAPKEPPSAFFLFCSEYRPK.....QPYEKKAALKKEKYEIDAA 69

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	370	100.0	178	2	Q8C7C4_MOUSE	Q8C7c4 mus musculus
2	370	100.0	180	1	HMGI_CRIGR	P07156 cricetus
3	370	100.0	181	2	Q8BNM0_MOUSE	Q8bnm0 mus musculus
4	370	100.0	192	2	Q5T7C5_HUMAN	Q5t7c5 homo sapien
5	370	100.0	214	1	HMGI_BOVIN	P10103 bos taurus
6	370	100.0	214	1	HMGI_CANFA	Q6yka4 canis famil
7	370	100.0	214	1	HMGI_HUMAN	P09429 homo sapien
8	370	100.0	214	1	HMGI_MOUSE	P63158 mus musculus
9	370	100.0	214	1	HMGI_RAT	P63159 rattus norv
10	370	100.0	215	2	Q5T7C3_HUMAN	Q5t7c3 homo sapien
11	370	100.0	215	2	Q4R844_MACFA	Q4r844 macaca fasc
12	370	100.0	215	2	Q88611_SPAEH	Q88611 spalax leuc
13	370	100.0	215	2	Q88612_SPAEH	Q88612 spalax leuc
14	370	100.0	215	2	Q9QWY6_SPAEH	Q9qwy6 spalax leuc
15	370	100.0	215	2	Q9QX40_SPAEH	Q9qx40 spalax leuc
16	370	100.0	215	2	Q548R9_RAT	Q548r9 rattus norv
17	370	100.0	215	2	Q58EV5_MOUSE	Q58ev5 m high mobi
18	366	98.9	214	2	Q9PUK9_CHICK	Q9pu9 gallus gall
19	366	98.9	215	2	Q9YH06_CHICK	Q9yh06 gallus gall
20	365	98.6	214	1	HMGI_PIG	P14321 sus scrofa
21	365	98.6	215	2	Q14321_HUMAN	Q14321 homo sapien
22	364	98.4	215	2	Q6P202_MOUSE	Q6p202 mus musculus
23	360	97.3	215	2	Q8BQ02_MOUSE	Q8bq02 mus musculus
24	359	97.0	206	2	Q5BKQ1_MOUSE	Q5bkq1 mus musculus
25	356	96.2	211	1	HMGI_HUMAN	Q9ugv6 homo sapien
26	355	95.9	211	1	Q9NQJ4_HUMAN	Q9nqj4 homo sapien
27	352	95.1	157	2	Q5T7C2_HUMAN	Q5t7c2 homo sapien
28	352	95.1	158	2	Q5T7C4_HUMAN	Q5t7c4 homo sapien
29	352	95.1	176	2	Q59GM1_HUMAN	Q59gm1 homo sapien
30	341	92.2	211	2	Q6P4N5_XENTR	Q6p4n5 xenopus tro
31	337	91.1	211	2	Q7S242_XENLA	Q7s242 xenopus lae

RESULT 1					
Q8C7C4_MOUSE					
ID	Q8C7C4_MOUSE	PRELIMINARY;	PRT;	178	AA.
AC	Q8C7C4;				
DC	01-MAR-2003	(Tremblrel. 23, Created)			
DT	01-MAR-2003	(Tremblrel. 23, Last sequence update)			
DT	01-MAR-2004	(Tremblrel. 26, Last annotation update)			
DE	Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C92030E14 product:high mobility group box 1, full insert sequence. (Fragment).				
DE	box 1, full insert sequence. (Fragment).				
GN	Name=Hmgbl;				
OS	Mus musculus (Mouse)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC	Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE				
RC	STRAIN=C57BL/6J; TISSUE=Thymus;				
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
RA	Carninci P., Hayashizaki Y.;				
RT	"High-efficiency full-length cDNA cloning."				
RL	Meth. Enzymol. 303:19-44(1999).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE				
RC	STRAIN=C57BL/6J; TISSUE=Thymus;				
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schriml L.M., Staubli P., Suzuki R., Tonita M., Wagner L., Washio T.,				
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,				
RA	Hayashizaki Y.;				
RT	"Functional annotation of a full-length mouse cDNA collection."				
RL	Nature 409:685-690(2001).				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE				
RC	STRAIN=C57BL/6J; TISSUE=Thymus;				
RA	The FANTOM Consortium,				
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."				

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RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kusunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK050659; BAC34367.1; -; mRNA.
DR HSSP; P07156; 1NHN.
DR SMR; Q8C7C4; 2-84; 93-171.
DR MGI; MGI:96113; Hmgbl.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0003023; F:nitric-oxide synthase regulator activity; IDA.
DR GO; GO:0005515; F:protein binding; IPT.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0006810; P:transport; IDA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS00118; HMG_BOX_2; 2.
FT NON_TER 178
FT SEQUENCE 178 AA; 20303 MW; 155FD80D52960A62 CRC64;
SQ
Query Match 100.0%; Score 370; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.4e-31;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADKQPEYKKAUK 60
Db |||||
QY 61 EYKQDIAA 69
Db |||||
Db 153 EYKQDIAA 161
RESULT 2

```

```

HMG1_CRIGR
ID HMG1_CRIGR STANDARD; PRT; 180 AA.
AC P07156;
DT 01-APR-1998 (Rel. 07, Created)
DT 01-APR-1998 (Rel. 07, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE High mobility group protein 1 (HMG-1) (High mobility group protein B1)
DE (Fragment).
OS Name=HMG1; Synonyms=HMG-1, HMG1;
OS Crictetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetidae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=87259986; PubMed=3601666;
RA Lee K.-L.D., Pentecost B.T., D'Anna J.A., Tobey R.A., Gurley L.R.,
RA Dixon G.H.;
RT "Characterization of cDNA sequences corresponding to three distinct
RT HMG-1 mRNA species in line CHO Chinese hamster cells and cell cycle
RT expression of the HMG-1 gene.";
RL Nucleic Acids Res. 15:5051-5068(1987).
RN [2]
RP STRUCTURE BY NMR OF 57-136.
RX MEDLINE=93347974; PubMed=8346022;
RA Read C.M., Cary P.D., Crane-Robinson C., Driscoll P.C., Norman D.G.;
RT "Solution structure of a DNA-binding domain from HMG1.";
RL Nucleic Acids Res. 21:3427-3436(1993).
CC -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC double stranded DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC -----
CC This Swiss-prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Y00365; CAA68441.1; -; Genomic_DNA.
DR PIR; A27853; A27853.
DR PDB; 1HSM; NMR; @=58-136.
DR PDB; 1HSN; NMR; @=58-136.
DR PDB; 1NHM; NMR; @=58-136.
DR PDB; 1NHN; NMR; @=58-136.
DR SMR; P07156; 1-49.
DR GO; GO:0000793; C:condensed chromosome; ISS.
DR GO; GO:0008301; F:DNA bending activity; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0006288; P:base-excision repair; DNA ligation; ISS.
DR GO; GO:0006310; P:DNA recombination; ISS.
DR GO; GO:0006281; P:DNA repair; ISS.
DR GO; GO:0006268; P:DNA unwinding; ISS.
DR GO; GO:0006325; P:establishment and/or maintenance of chromatin; ISS.
DR GO; GO:0017055; P:negative regulation of transcriptional preinitiation; ISS.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS00118; HMG_BOX_2; 2.
KW 3D-structure; Chromosomal protein; DNA-binding; Nuclear protein;
KW Repeat.
FT DNA_BIND <1 44 HMG box 1.
FT DNA_BIND 60 128 HMG box 2.
FT COMBIAS 151 180 Asp/Glu-rich (acidic).
FT NON_TER 1 1
FT HELIX 67 81
FT TURN 83 84
FT TURN 87 88

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ID Q5T7C5_HUMAN PRELIMINARY; PRT; 192 AA.
AC Q5T7C5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE High-mobility group box 1 (fragment).
GN Name=HMGb1; ORFNames=RP11-550P23.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pellan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL353648; CAIL5602.1; -; Genomic_DNA.
DR SMR; Q5T7C5; 2-84, 93-171.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000335; Highmoblty_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBLTY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS50118; HMG_BOX_2; 2.
FT NON TER 192
FT SEQUENCE 192 AA; 22050 MW; 6A52DB61DA307C1D CRC64;

Query Match 100.0%; Score 370; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-31;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 60
Db |||||
93 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 152

QY 61 EYKXDIAA 69
Db |||||
153 EYKXDIAA 161

RESULT 5
HMG1_BOVIN
ID HMG1_BOVIN STANDARD; PRT; 214 AA.
AC P10103;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE High mobility group protein 1 (HMG-1) (High mobility group protein
DE B1).
GN Name=HMGb1; Synonyms=HMG1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Holstein; TISSUE=Fetal thymus;
RX MEDLINE=89057489; PubMed=3194213;
RA Kaplan D.J.; Duncan C.H.;
RT "Full length cDNA sequence for bovine high mobility group 1 (HMG1)
RT protein.";
RL Nucleic Acids Res. 16:10375-10375 (1988).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 115-214.
RX MEDLINE=84128872; PubMed=6141822;
RA Pentecost B.; Dixon G.H.;
RT "Isolation and partial sequence of bovine cDNA clones for the high-
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RT mobility-group protein (HMG-1).";
RL Biosci. Rep. 4:49-57 (1984).
RN [3]
RP PROTEIN SEQUENCE OF 1-37; 45-156 AND 158-194.
RX MEDLINE=81138848; PubMed=7202717; DOI=10.1016/0014-5793(80)80453-4;
RA Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.;
RT "The primary structures of non-histone chromosomal proteins HMG 1 and
RT 2.";
RL FEBS Lett. 122:264-270 (1980).
RN [4]
RP PROTEIN SEQUENCE OF 1-36.
RX MEDLINE=90306387; PubMed=2365081; DOI=10.1016/0014-5793(90)80308-6;
RA Christen T., Bischoff M., Hobi R., Kuenzle C.C.;
RT "High mobility group proteins 1 and 2 bind preferentially to
RT brominated poly(dG-dC) poly(dG-dC) in the Z-DNA conformation but not
RT to other types of Z-DNA.";
RL FEBS Lett. 267:139-141 (1990).
CC -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC double stranded DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X12796; CAA31284.1; -; mRNA.
DR EMBL; M26110; AAA30567.1; -; mRNA.
DR PIR; S01947; S01947.
DR HSSP; P07156; 1NHN.
DR SMR; P10103; 1-83, 92-170.
DR GO; GO:0000793; C:condensed chromosome; ISS.
DR GO; GO:0008301; F:DNA bending activity; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0006289; P:base-excision repair, DNA ligation; ISS.
DR GO; GO:0006310; P:DNA recombination; ISS.
DR GO; GO:0006281; P:DNA repair; ISS.
DR GO; GO:0006268; P:DNA unwinding; ISS.
DR GO; GO:0006325; P:establishment and/or maintenance of chromat. .; ISS.
DR GO; GO:0017055; P:negative regulation of transcriptional prel. .; ISS.
DR InterPro; IPR001335; Highmoblty_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBLTY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS50118; HMG_BOX_2; 2.
KW Chromosomal protein; Direct protein sequencing; DNA-binding;
KW Nuclear protein; Repeat.
FT INIT MET 0
FT DNA_BIND 8 78 HMG box 1.
FT DNA_BIND 94 162 HMG box 2.
FT COMBIAS 185 214 Asp/Glu-rich (acidic).
FT CONFLICT 22 22 C -> S (in Ref. 3).
FT CONFLICT 105 105 C -> A (in Ref. 3).
FT CONFLICT 115 119 EHPGL -> PGGGV (in Ref. 2).
FT CONFLICT 193 193 E -> D (in Ref. 3).
FT SEQUENCE 214 AA; 24777 MW; B283A80FC7F0F433 CRC64;

Query Match 100.0%; Score 370; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 60
Db |||||
92 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 151

QY 61 EYKXDIAA 69
Db |||||
152 EYKXDIAA 160
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RESULT 6
HMGI_CANFA
ID HMGI CANFA STANDARD; PRT; 214 AA.
AC Q6YK44;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE High mobility group protein 1 (HMG-1) (High mobility group protein
DE B1).
GN Name=HMG1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
RX MEDLINE=22932580; PubMed=14571134; DOI=10.1159/000073415;
RA Murua Escobar H., Meyer B., Richter A., Becker K., Flohr A.M.,
RA Bullerdiek J., Nolte I.;
RT "Molecular characterization of the canine HMG1.";
RL Cytogenet. Genome Res. 101:33-38(2003).
CC -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC double stranded DNA (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AY135519; AAN11296.1; -; mRNA.
DR EMBL; AY135521; AAN11319.1; -; Genomic DNA.
DR HSSP; P07155; 1AAB.
DR SMR; Q6YK44; 1-83, 92-170.
DR Ensembl; ENSCAFG0000006597; Canis familiaris.
DR InterPro; IPR000135; Highmoblty_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBLTY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS0118; HMG_BOX_2; 2.
KW Chromosomal protein; DNA-Binding; Nuclear protein; Repeat.
FT INIT_MET 0 By similarity.
FT DNA_BIND 8 78 HMG box 1.
FT DNA_BIND 94 162 HMG box 2.
FT COMBIAS 185 214 Asp/Glu-rich (acidic).
SQ SEQUENCE 214 AA; 24763 MW; B3C6A80FC7F0F433 CRC64;

Query Match 100.0%; Score 370; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKPPSAFFLFCSEYRPKTGEHPGLSIGDVAKLGEWMNNTAADKQPYEKKAALK 60
Db 92 NAPKPPSAFFLFCSEYRPKTGEHPGLSIGDVAKLGEWMNNTAADKQPYEKKAALK 151

Qy 61 EYKEDIAA 69
Db 152 EYKEDIAA 160

RESULT 7
HMGI_HUMAN
ID HMGI HUMAN STANDARD; PRT; 214 AA.
AC P09429; Q6IBEL;
DT 01-MAR-1989 (Rel. 10, Created)

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DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE High mobility group protein 1 (HMG-1) (High mobility group protein
DE B1).
GN Name=HMG1; Synonyms=HMGI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=89160247; PubMed=2922262;
RA Wen L., Huang J.K., Johnson B.H., Reeck G.R.;
RT "A human placental cDNA clone that encodes nonhistone chromosomal
RT protein HMG-1.";
RL Nucleic Acids Res. 17:1197-1214(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;
RA Ferrari S., Finelli P., Rocchi M., Bianchi M.E.;
RT "The active gene that encodes human high mobility group 1 protein
RT (HMG1) contains introns and maps to chromosome 13.";
RL Genomics 35:367-371(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA He F.T., Yang Z.H., Ji Q., Li R., Peng J., Jiang Y., Zhong X.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Small intestine;
RG The German cDNA consortium;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
RT vector (pDONR201).";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain, Cervix, and Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP PROTEIN SEQUENCE OF 57-64 AND 112-126.

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RC TISSUE=Mammary carcinoma;  
RX MEDLINE=97295304; PubMed=9150946;  
RA Ramussen R.K., Ji H., Edes J.S., Moritz R.L., Reid G.E.,  
RT Simpson R.J., Dorow D.S.;  
RT "Two-dimensional electrophoretic analysis of human breast carcinoma  
RT proteins: mapping of proteins that bind to the SH3 domain of mixed  
RT lineage kinase MLK2.";  
RL Electrophoresis 18:588-598(1997).  
CC -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds  
CC double stranded DNA.  
CC -!- INTERACTION:  
CC P04637:TP53; IntAct=EBI-389432, EBI-366083;  
CC O15350:TP73; NExp=1; IntAct=EBI-389432, EBI-389606;  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: Belongs to the HMGI/HMG2 protein family.  
CC -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.  
CC -----  
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; X12597; CAA31110.1; -; mRNA.  
DR EMBL; U51677; AAB08987.1; -; Genomic DNA.  
DR EMBL; AY377859; AAQ91389.1; -; mRNA.  
DR EMBL; CR749614; CAH18408.1; -; mRNA.  
DR EMBL; CR456863; CAG33144.1; -; mRNA.  
DR EMBL; BT006940; AAP35586.1; -; mRNA.  
DR EMBL; BT020159; AAV38961.1; -; mRNA.  
DR EMBL; BC003378; AAH03378.1; -; mRNA.  
DR EMBL; BC030981; AAH03098.1; -; mRNA.  
DR EMBL; BC068889; AAH68889.1; -; mRNA.  
DR EMBL; BC067732; AAH67732.1; -; mRNA.  
DR PIR; S02826; S02826.  
DR HSSP; P07156; 1NHX.  
DR SMR; P09429; 1-83, 92-170.  
DR IntAct; P09429; -.  
DR Ensembl; ENSG00000189403; Homo sapiens.  
DR HGNC; HGNC:4983; HMGB1.  
DR H-InvDB; HIX0011209; -.  
DR MIM; 163905; -.  
DR GO; GO:0000793; C:condensed chromosome; IDA.  
DR GO; GO:0008301; F:DNA bending activity; TAS.  
DR GO; GO:0008134; P:transcription factor binding; TAS.  
DR GO; GO:0006288; P:base-excision repair, DNA ligation; IDA.  
DR GO; GO:0006310; P:DNA recombination; TAS.  
DR GO; GO:0006281; P:DNA repair; TAS.  
DR GO; GO:0006268; P:DNA unwinding; NAS.  
DR GO; GO:0006325; P:establishment and/or maintenance of chromatin; TAS.  
DR GO; GO:0006357; P:negative regulation of transcriptional preinitiation; IDA.  
DR InterPro; IPR000135; Highmobility 12.  
DR InterPro; IPR000910; HMG 12\_box.  
DR Pfam; PF00505; HMG box; 2.  
DR PRINTS; PR00886; HIGHMOB1Y12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS00353; HMG BOX 1; 1.  
DR PROSITE; PS01118; HMG BOX 2; 2.  
KW Chromosomal protein; Direct protein sequencing; DNA-binding;  
KW Nuclear protein; Repeat.  
FT INIT MET 0 0  
FT DNA\_BIND 8 78 HMG box 1.  
FT DNA\_BIND 94 162 HMG box 2.  
FT COMBIPAS 185 214 Asp/Glu-rich (acidic).  
FT CONFLICT 214 214 E -> D (in Ref. 5).  
SQ SEQUENCE 214 AA; 24763 MW; B3C6A80FC7F0F433 CRC64;  
Query Match 100.0%; Score 370; DB 1; Length 214;  
Best Local Similarity 100.0%; Pred. No. 1.7e-31;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 NAPKRPPSAFFLCSEYRPKIKGHPGLSIGDVAKLGMWNTAADDQKPYEKKAALK 60

Db 92 NAPKRPPSAFFLCSEYRPKIKGHPGLSIGDVAKLGMWNTAADDQKPYEKKAALK 151  
QY 61 EKYEKDIAA 69  
Db 152 EKYEKDIAA 160  
RESULT 8  
HMGI\_MOUSE  
ID HMGI\_MOUSE STANDARD; PRT; 214 AA.  
AC P63158; P07155; P27109; P27428;  
DT 01-APR-1988 (Rel. 07, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE High mobility group protein 1 (HMG-1) (high mobility group protein  
DE B1).  
GN Name=Hmgbl; Synonyms=Hmg-1, Hmg1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C3H/He;  
RX MEDLINE=92335012; PubMed=1630928;  
RA Yotov W.V., St Arnaud R.;  
RT "Nucleotide sequence of a mouse cDNA encoding the nonhistone  
RT chromosomal high mobility group protein-1 (HMG1).";  
RN Nucleic Acids Res. 20:3516-3516(1992).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;  
RA Pauken C.M., Nagle D.L., Bucan M., Lo C.W.;  
RT "Molecular cloning, expression analysis, and chromosomal localization  
RT of mouse Hmg1-containing sequences.";  
RN Mamm. Genome 5:91-99(1994).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/SV; TISSUE=Liver;  
RX MEDLINE=95050689; PubMed=7961836;  
RA Ferrari S., Ronfani L., Calogero S., Bianchi M.;  
RT "The mouse gene coding for high mobility group 1 protein (HMG1).";  
RN J. Biol. Chem. 269:28803-28808(1994).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=AKR/J;  
RA Ghosh B.;  
RN Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).





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DR EMBL; Y00463; CAA68526.1; -; mRNA.
DR EMBL; BC061779; AAH61779.1; -; mRNA.
DR EMBL; BC081839; AAH81839.1; -; mRNA.
DR EMBL; BC088402; AAH88402.1; -; mRNA.
DR PIR; A41175; NSRTH1.
DR PDB; 1AAB; NMR; @=1-83.
DR PDB; 1CKT; X-ray; A=7-77.
DR PDB; 1HME; NMR; @=88-164.
DR PDB; 1HMF; NMR; @=88-164.
DR SMR; P63159; 1-83, 92-170.
DR Ensemble; ENSNRG00000030351; Rattus norvegicus.
DR RGD; 2802; Hmgb1.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBLTV12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS0118; HMG_BOX_2; 2.
DR 3D-structure; Chromosomal protein; Direct protein sequencing;
KW DNA-binding; Heparin-binding; Nuclear protein; Repeat.
FT INIT MET 0 0
FT DNA_BIND 8 78 HMG box 1.
FT DNA_BIND 94 162 HMG box 2.
FT COMEBIAS 185 214 Asp/Glu-rich (acidic).
FT HELIX 14 29
FT TURN 31 32
FT HELIX 37 49
FT TURN 50 50
FT TURN 53 55
FT HELIX 57 74
FT TURN 75 76
FT HELIX 100 115
FT TURN 117 118
FT HELIX 121 134
FT HELIX 137 158
FT TURN 159 160
FT SEQUENCE 214 AA; 24763 MW; B3C6A91FD6F1B133 CRC64;

Query Match 100.0%; Score 370; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKRPSPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
DB 92 NAKRPSPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 151

QY 61 EKYKDIAA 69
DB 152 EKYKDIAA 160

RESULT 10
Q577C3_HUMAN PRELIMINARY; PRT; 215 AA.
AC Q577C3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE High-mobility group box 1.
GN Name=HMGb1; ORFNames=RP11-550P23.1-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL353648; CA115600.1; -; Genomic_DNA.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;

Query Match 100.0%; Score 370; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKRPSPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
DB 93 NAKRPSPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

QY 61 EKYKDIAA 69
DB 153 EKYKDIAA 161

RESULT 12
O88611_SPAEH PRELIMINARY; PRT; 215 AA.
AC O88611;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE High mobility group protein.
GN Name=HMG1;
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Spalacinae; Nannospalax.

DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;

Query Match 100.0%; Score 370; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKRPSPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
DB 93 NAKRPSPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

QY 61 EKYKDIAA 69
DB 153 EKYKDIAA 161

RESULT 12
O88611_SPAEH PRELIMINARY; PRT; 215 AA.
AC O88611;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE High mobility group protein.
GN Name=HMG1;
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Spalacinae; Nannospalax.

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OX NCBI_TaxID=30637;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee K.-L.D., Lum H.-K., Nevo E.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF078817; AAC27650.2; -; Genomic_DNA.
DR HSSP; P07156; 1NHN.
DR SMR; O88611; 2-84, 93-171.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS0118; HMG_BOX_2; 2.
SQ SEQUENCE 215 AA; 24905 MW; 64816B6FCF6033EA CRC64;

Query Match 100.0%; Score 370; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 60
Db 93 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 152

QY 61 EYKEDIAA 69
Db 153 EYKEDIAA 161

RESULT 13
ID O88612 SPAEH PRELIMINARY; PRT; 215 AA.
AC O88612
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE High mobility group protein.
GN Name=HMG1;
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Spalacinae; Nannospalax.
OX NCBI_TaxID=30637;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee K.-L.D., Lum H.-K., Nevo E.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF078818; AAC27651.1; -; Genomic_DNA.
DR HSSP; P07156; 1NHN.
DR SMR; O88612; 2-84, 93-171.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS0118; HMG_BOX_2; 2.
SQ SEQUENCE 215 AA; 24923 MW; 1C6FB6845CA1B6C8 CRC64;

Query Match 100.0%; Score 370; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 60
Db 93 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 152

QY 61 EYKEDIAA 69
Db 153 EYKEDIAA 161

RESULT 14
ID O9QWY6 SPAEH PRELIMINARY; PRT; 215 AA.
AC O9QWY6
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE High mobility group protein.
GN Name=HMG1;
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Spalacinae; Nannospalax.
OX NCBI_TaxID=30637;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee K.-L.D., Lum H.-K., Nevo E.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF078819; AAC27652.1; -; Genomic_DNA.
DR HSSP; P07156; 1NHN.
DR SMR; O9QWY6; 2-84, 93-171.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS0118; HMG_BOX_2; 2.
SQ SEQUENCE 215 AA; 24822 MW; D20D659274B575B4 CRC64;

Query Match 100.0%; Score 370; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 60
Db 93 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 152

QY 61 EYKEDIAA 69
Db 153 EYKEDIAA 161

RESULT 15
ID Q9QX40 SPAEH PRELIMINARY; PRT; 215 AA.
AC Q9QX40
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE High mobility group protein.
GN Name=HMG1;
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Spalacinae; Nannospalax.
OX NCBI_TaxID=30637;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lee K.-L.D., Lum H.-K., Nevo E.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF078820; AAC27653.2; -; Genomic_DNA.
DR HSSP; P07156; 1NHN.
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DR SMR; Q9QX40; 2-84, 93-171.  
DR GO; GO:0000785; C:chromatin; IEA.  
DR GO; GO:005634; C:nucleus; IEA.  
DR CO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR000135; Highmoblty\_12.  
DR InterPro; IPR000910; HMG\_12\_box.  
DR Pfam; PF0505; HMG\_box; 2.  
DR PRINTS; PR00886; HIGHMOBLTY12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS00353; HMG\_BOX\_1; 1.  
DR PROSITE; PS0118; HMG\_BOX\_2; 2.  
SQ SEQUENCE 215 AA; 24895 MW; 599FB8A6FDF41F17 CRC64;  
  
Query Match 100.0%; Score 370; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.7e-31;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 NAPKPPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 60  
|||  
Db 93 NAPKPPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 152  
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Qy 61 EYKEDIAA 69  
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Db 153 EYKEDIAA 161  
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Job time : 82.4836 secs

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OM protein - protein search, using sw model

Run on: April 6, 2006, 10:25:39 ; Search time 19,7467 Seconds  
(without alignments)  
288.890 Million cell updates/sec

Title: US-10-717-984-5

Perfect score: 370

Sequence: 1 NAPKPPSAFFLFCSEYRPK.....QPVEKKAALKKEYEKIDIAA 69

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/PTUS COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	214	2 US-09-538-092-883	Sequence 883, App
2	370	100.0	214	2 US-09-214-881A-1	Sequence 1, Appli
3	370	100.0	214	2 US-09-214-881A-3	Sequence 3, Appli
4	365	98.6	214	2 US-09-214-881A-4	Sequence 4, Appli
5	365	98.6	214	2 US-09-214-881A-5	Sequence 5, Appli
6	356	96.2	213	2 US-09-949-016-10813	Sequence 10813, A
7	324	87.6	208	2 US-09-538-092-1018	Sequence 1018, Ap
8	324	87.6	208	2 US-09-214-881A-2	Sequence 2, Appli
9	324	87.6	209	2 US-09-214-881A-6	Sequence 6, Appli
10	324	87.6	209	2 US-09-214-881A-8	Sequence 8, Appli
11	324	87.6	320	2 US-09-949-016-10728	Sequence 10728, A
12	321	86.8	206	2 US-09-214-881A-9	Sequence 9, Appli
13	317	85.7	879	2 US-09-914-259-38	Sequence 38, Appl
14	300	81.1	201	2 US-09-214-881A-10	Sequence 10, Appl
15	294	79.5	200	2 US-09-702-705-324	Sequence 324, App
16	294	79.5	200	2 US-09-702-705-789	Sequence 789, App
17	294	79.5	200	2 US-09-736-457-324	Sequence 324, App
18	294	79.5	200	2 US-09-736-457-789	Sequence 789, App
19	294	79.5	200	2 US-09-614-124B-324	Sequence 324, App
20	294	79.5	200	2 US-09-614-124B-789	Sequence 789, App
21	294	79.5	200	2 US-09-671-325-324	Sequence 324, App
22	294	79.5	200	2 US-09-671-325-789	Sequence 789, App
23	294	79.5	200	2 US-09-589-184-324	Sequence 324, App
24	294	79.5	200	2 US-09-589-184-789	Sequence 789, App
25	294	79.5	200	2 US-09-658-824-324	Sequence 324, App
26	294	79.5	200	2 US-09-658-824-789	Sequence 789, App
27	294	79.5	200	2 US-10-017-754-324	Sequence 324, App

28	294	79.5	200	2 US-10-017-754-789	Sequence 789, App
29	294	79.5	200	2 US-09-651-563-324	Sequence 324, App
30	294	79.5	200	2 US-09-651-563-789	Sequence 789, App
31	294	79.5	200	2 US-09-519-642-324	Sequence 324, App
32	294	79.5	200	2 US-09-519-642-789	Sequence 789, App
33	294	79.5	207	2 US-09-702-705-1667	Sequence 1667, Ap
34	294	79.5	207	2 US-09-736-457-1667	Sequence 1667, Ap
35	294	79.5	207	2 US-09-614-124B-1667	Sequence 1667, Ap
36	294	79.5	207	2 US-09-671-325-1667	Sequence 1667, Ap
37	294	79.5	207	2 US-09-658-824-1667	Sequence 1667, Ap
38	294	79.5	207	2 US-10-017-754-1667	Sequence 1667, Ap
39	294	79.5	207	2 US-10-017-754-1913	Sequence 1913, Ap
40	294	79.5	207	2 US-09-651-563-1667	Sequence 1667, Ap
41	294	79.5	208	2 US-09-214-881A-11	Sequence 11, Appl
42	294	79.5	228	2 US-09-949-016-10496	Sequence 10496, A
43	292	78.9	185	2 US-09-214-881A-7	Sequence 7, Appli
44	170	45.9	709	1 US-07-814-964-7	Sequence 7, Appli
45	170	45.9	709	1 US-08-258-442-7	Sequence 7, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-538-092-883  
; Sequence 883, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; APPLICANT: Mansfield, Traci A.  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CuraPatSeqformat Version 0.9  
; SEQ ID NO 883  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Polypeptide Accession Number P09429  
US-09-538-092-883

Query Match 100.0%; Score 370; DB 2; Length 214;

Best Local Similarity 100.0%; Pred. No. 3.1e-40;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	NAPKPPSAFFLFCSEYRPKIGEHPLSGVAKLGEWMNTAADDKQPYEKKAAKLK 60
Db	92	NAPKPPSAFFLFCSEYRPKIGEHPLSGVAKLGEWMNTAADDKQPYEKKAAKLK 151
Qy	61	EKYEKIDIAA 69
Db	152	EKYEKIDIAA 160

##### RESULT 2

US-09-214-881A-1  
; Sequence 1, Application US/09214881A  
; Patent No. 6822078  
; GENERAL INFORMATION:  
; APPLICANT: Ozaki, Shoichi  
; APPLICANT: Sobajima, Junko  
; APPLICANT: Uesugi, Hiroko  
; APPLICANT: Okazaki, Takahiro  
; APPLICANT: Tanaka, Masao

```

; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-1

Query Match          100.0%; Score 370; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.1e-40;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 60
Db 92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 151

QY 61 EYKEDIAA 69
Db 152 EYKEDIAA 160

RESULT 3
US-09-214-881A-3
; Sequence 3, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-214-881A-3

Query Match          100.0%; Score 370; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.1e-40;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 60
Db 92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 151

QY 61 EYKEDIAA 69
Db 152 EYKEDIAA 160

RESULT 4
US-09-214-881A-4
; Sequence 4, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:

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; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-214-881A-4

Query Match          98.6%; Score 365; DB 2; Length 214;
Best Local Similarity 98.6%; Pred. No. 1.4e-39;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 60
Db 92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 151

QY 61 EYKEDIAA 69
Db 152 EYKEDIAA 160

RESULT 5
US-09-214-881A-5
; Sequence 5, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-214-881A-5

Query Match          98.6%; Score 365; DB 2; Length 214;
Best Local Similarity 98.6%; Pred. No. 1.4e-39;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 60
Db 92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 151

QY 61 EYKEDIAA 69
Db 152 EYKEDIAA 160

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RESULT 6
US-09-949-016-10813
; Sequence 10813, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 10813
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10813

Query Match          96.6%; Score 356; DB 2; Length 213;
Best Local Similarity 97.1%; Pred. No. 2.1e-38;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NAPKRPSPAFFLFCSEYRPRKIGEHPLGLSGDVAKKLGEMWNNTAADDKOPYEKKAAKLK 60
Db 95 NAPKRPSPAFFLFCSEYRPRKIGEHPLGLSGDVAKKLGEMWNNTAADDKOPYEKKAAKLK 154

QY 61 EYKEDIAA 69
Db 155 EYKEDIAA 163

RESULT 7
US-09-538-092-1018
; Sequence 1018, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 1018
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018

Query Match          87.6%; Score 324; DB 2; Length 208;
Best Local Similarity 87.0%; Pred. No. 3e-34;
Matches 60; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 NAPKRPSPAFFLFCSEYRPRKIGEHPLGLSGDVAKKLGEMWNNTAADDKOPYEKKAAKLK 60
Db 92 NAPKRPSPAFFLFCSEYRPRKIGEHPLGLSGDTAKKLGEMWSEQSAKDKOPYEQKAAKLK 151

RESULT 8
US-09-214-881A-2
; Sequence 2, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-2

Query Match          87.6%; Score 324; DB 2; Length 208;
Best Local Similarity 87.0%; Pred. No. 3e-34;
Matches 60; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 NAPKRPSPAFFLFCSEYRPRKIGEHPLGLSGDVAKKLGEMWNNTAADDKOPYEKKAAKLK 60
Db 92 NAPKRPSPAFFLFCSEYRPRKIGEHPLGLSGDTAKKLGEMWSEQSAKDKOPYEQKAAKLK 151

RESULT 9
US-09-214-881A-6
; Sequence 6, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-214-881A-6

Query Match          87.6%; Score 324; DB 2; Length 209;
Best Local Similarity 87.0%; Pred. No. 3e-34;
Matches 60; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 10:26:34 ; Search time 65.5954 Seconds  
(without alignments)  
439.516 Million cell updates/sec

Title: US-10-717-984-5

Perfect score: 370

Sequence: 1 NAPKRPSPAFFLFCSEYRPK.....QPVEKKAALKKEYEKIDIAA 69

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*  
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2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pap:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	69	4	US-10-147-447-5
2	370	100.0	69	4	US-10-300-072-5
3	370	100.0	69	4	US-10-456-949-5
4	370	100.0	69	4	US-10-456-947-5
5	370	100.0	69	4	US-10-456-947-5
6	370	100.0	69	4	US-10-456-947-5
7	370	100.0	74	4	US-10-300-072-51
8	370	100.0	74	4	US-10-456-947-37
9	370	100.0	74	4	US-10-718-495-51
10	370	100.0	74	4	US-10-717-984-51
11	370	100.0	74	5	US-10-938-992-67
12	370	100.0	74	5	US-10-938-992-76
13	370	100.0	92	4	US-10-300-072-58
14	370	100.0	92	4	US-10-456-947-43
15	370	100.0	92	4	US-10-718-495-58
16	370	100.0	92	4	US-10-717-984-58
17	370	100.0	92	5	US-10-938-992-73
18	370	100.0	98	4	US-10-424-599-211221
19	370	100.0	128	3	US-09-925-300-1757
20	370	100.0	176	4	US-10-094-749-2948
21	370	100.0	180	5	US-10-938-992-36
22	370	100.0	214	3	US-09-214-881A-1
23	370	100.0	214	3	US-09-214-881A-3
24	370	100.0	214	5	US-10-726-195-1
25	370	100.0	214	5	US-10-726-195-3
26	370	100.0	215	4	US-10-087-192-1446
27	370	100.0	215	4	US-10-147-447-1

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28 370 100.0 215 4 US-10-147-447-2 Sequence 2, Appli
29 370 100.0 215 4 US-10-300-072-1 Sequence 1, Appli
30 370 100.0 215 4 US-10-300-072-2 Sequence 2, Appli
31 370 100.0 215 4 US-10-456-949-1 Sequence 1, Appli
32 370 100.0 215 4 US-10-456-949-2 Sequence 2, Appli
33 370 100.0 215 4 US-10-456-947-1 Sequence 1, Appli
34 370 100.0 215 4 US-10-456-947-2 Sequence 2, Appli
35 370 100.0 215 4 US-10-718-495-1 Sequence 1, Appli
36 370 100.0 215 4 US-10-718-495-2 Sequence 2, Appli
37 370 100.0 215 4 US-10-717-984-1 Sequence 1, Appli
38 370 100.0 215 4 US-10-717-984-2 Sequence 2, Appli
39 370 100.0 215 5 US-10-868-577A-63 Sequence 63, Appli
40 370 100.0 215 5 US-10-868-549-22 Sequence 22, Appli
41 370 100.0 215 5 US-10-938-992-18 Sequence 18, Appli
42 370 100.0 215 5 US-10-938-992-38 Sequence 38, Appli
43 370 100.0 215 5 US-10-938-992-74 Sequence 74, Appli
44 370 100.0 220 4 US-10-087-192-1443 Sequence 1443, Ap
45 370 100.0 221 5 US-10-938-992-40 Sequence 40, Appli

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## ALIGNMENTS

## RESULT 1

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US-10-147-447-5
; Sequence 5, Application US/10147447
; Publication No. US20030060410A1
; GENERAL INFORMATION:
; APPLICANT: Tracey, Kevin J.
; APPLICANT: Yang, Huan
; APPLICANT: Warren Jr., Howland Shaw
; APPLICANT: Fink, Mitchell P.
; TITLE OF INVENTION: Use of HMG Fragments as
; FILE REFERENCE: 3268.1001-001
; CURRENT APPLICATION NUMBER: US/10/147,447
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-147-447-5

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Query Match 100.0%; Score 370; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.5e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 60
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Db 1 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 60
    |||||
QY 61 EYKEDIAA 69
    |||||
Db 61 EYKEDIAA 69
    |||||

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## RESULT 2

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US-10-300-072-5
; Sequence 5, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; APPLICANT: Howland Shaw Warren, Jr.
; APPLICANT: Mitchell P. Fink
; TITLE OF INVENTION: USE OF HMG FRAGMENTS AS ANTI-FLAMMATORY
; FILE REFERENCE: 3268.1001-005
; CURRENT APPLICATION NUMBER: US/10/300,072

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; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-072-5

Query Match      100.0%; Score 370; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.5e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60
Db 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60

QY 61 EYKEDIAA 69
Db 61 EYKEDIAA 69

RESULT 3
US-10-456-949-5
; Sequence 5, Application US/10456949
; Publication No. US2004005316A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
; FILE REFERENCE: 3268.1001-006
; CURRENT APPLICATION NUMBER: US/10/456,949
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-456-949-5

Query Match      100.0%; Score 370; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.5e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60
Db 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60

QY 61 EYKEDIAA 69
Db 61 EYKEDIAA 69

RESULT 4
US-10-456-947-5
; Sequence 5, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMBG POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS

```

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; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456,947
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mouse/ rat/ human
US-10-456-947-5

Query Match      100.0%; Score 370; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.5e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60
Db 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60

QY 61 EYKEDIAA 69
Db 61 EYKEDIAA 69

RESULT 5
US-10-718-495-5
; Sequence 5, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; TITLE OF INVENTION: USE OF HMBG FRAGMENTS AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3258.1009-001
; CURRENT APPLICATION NUMBER: US/10/718,495
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/427,841
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-718-495-5

Query Match      100.0%; Score 370; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.5e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60
Db 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNTAADDKQPYEKKAAKLK 60

QY 61 EYKEDIAA 69
Db 61 EYKEDIAA 69

RESULT 6
US-10-717-984-5
; Sequence 5, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
; FILE REFERENCE: 3258.1008-001
; CURRENT APPLICATION NUMBER: US/10/717,984

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; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,846
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-717-984-5

Query Match
Best Local Similarity 100.0%; Score 370; DB 4; Length 69;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKLGEWNNNTAADDKQPYEKKAAKLK 60
Db 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKLGEWNNNTAADDKQPYEKKAAKLK 60
QY 61 EYKEDIAA 69
Db 61 EYKEDIAA 69

RESULT 7
US-10-300-072-51
; Sequence 51, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Howland Shaw Warren, Jr.
; APPLICANT: Mitchell P. Fink
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
; FILE REFERENCE: 3268.1001-005
; CURRENT APPLICATION NUMBER: US/10/300,072
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-072-51

Query Match
Best Local Similarity 100.0%; Score 370; DB 4; Length 74;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKLGEWNNNTAADDKQPYEKKAAKLK 60
Db 5 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKLGEWNNNTAADDKQPYEKKAAKLK 64
QY 61 EYKEDIAA 69
Db 65 EYKEDIAA 73

RESULT 8
US-10-456-947-37
; Sequence 37, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456,947
; CURRENT FILING DATE: 2003-06-06
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-456-947-37

Query Match
Best Local Similarity 100.0%; Score 370; DB 4; Length 74;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKLGEWNNNTAADDKQPYEKKAAKLK 60
Db 5 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKLGEWNNNTAADDKQPYEKKAAKLK 64
QY 61 EYKEDIAA 69
Db 65 EYKEDIAA 73

RESULT 9
US-10-718-495-51
; Sequence 51, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3258.1009-001
; CURRENT APPLICATION NUMBER: US/10/718,495
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/427,841
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-718-495-51

Query Match
Best Local Similarity 100.0%; Score 370; DB 4; Length 74;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKLGEWNNNTAADDKQPYEKKAAKLK 60
Db 5 NAPKPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKLGEWNNNTAADDKQPYEKKAAKLK 64
QY 61 EYKEDIAA 69
Db 65 EYKEDIAA 73

RESULT 10
US-10-717-984-51
; Sequence 51, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
; FILE REFERENCE: 3258.1008-001
; CURRENT APPLICATION NUMBER: US/10/717,984
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,846
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; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-717-984-51

Query Match      100.0%; Score 370; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 6e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
    |||||||
Db 5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64
    |||||||

QY 61 EYKEDIAA 69
    |||||||
Db 65 EYKEDIAA 73

RESULT 11
US-10-938-992-67
; Sequence 67, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-992-67

Query Match      100.0%; Score 370; DB 5; Length 74;
Best Local Similarity 100.0%; Pred. No. 6e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
    |||||||
Db 5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64
    |||||||

QY 61 EYKEDIAA 69
    |||||||
Db 65 EYKEDIAA 73

RESULT 12
US-10-938-992-76
; Sequence 76, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
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; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-992-76

Query Match      100.0%; Score 370; DB 5; Length 74;
Best Local Similarity 100.0%; Pred. No. 6e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
    |||||||
Db 5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64
    |||||||

QY 61 EYKEDIAA 69
    |||||||
Db 65 EYKEDIAA 73

RESULT 13
US-10-300-072-58
; Sequence 58, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; APPLICANT: Howland Shaw Warren, Jr.
; APPLICANT: Mitchell P. Fink
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 3268.1001-005
; CURRENT APPLICATION NUMBER: US/10/300,072
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-072-58

Query Match      100.0%; Score 370; DB 4; Length 92;
Best Local Similarity 100.0%; Pred. No. 7.8e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
    |||||||
Db 5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64
    |||||||

QY 61 EYKEDIAA 69
    |||||||
Db 65 EYKEDIAA 73

RESULT 14
US-10-456-947-43
; Sequence 43, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456,947
; CURRENT FILING DATE: 2003-06-06
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; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-456-947-43

Query Match      100.0%; Score 370; DB 4; Length 92;
Best Local Similarity 100.0%; Pred. No. 7.8e-37; Indels 0; Gaps 0;
Matches 69; Conservative 0; Mismatches 0;

QY 1 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNNTAADDKQPYEKKAALK 60
Db 5 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNNTAADDKQPYEKKAALK 64

QY 61 EYKEDIAA 69
Db 65 EYKEDIAA 73

RESULT 15
US-10-718-495-58
; Sequence 58, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3258.1009-001
; CURRENT APPLICATION NUMBER: US/10/718,495
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/427,841
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-718-495-58

Query Match      100.0%; Score 370; DB 4; Length 92;
Best Local Similarity 100.0%; Pred. No. 7.8e-37; Indels 0; Gaps 0;
Matches 69; Conservative 0; Mismatches 0;

QY 1 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNNTAADDKQPYEKKAALK 60
Db 5 NAPKRPSPAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNNTAADDKQPYEKKAALK 64

QY 61 EYKEDIAA 69
Db 65 EYKEDIAA 73

Search completed: April 6, 2006, 10:32:47
Job time : 66.5954 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

# OM protein - protein search, using sw model

Run on: April 6, 2006, 10:28:08 ; Search time 8.625 Seconds  
(without alignments)  
249.536 Million cell updates/sec

Title: US-10-717-984-5

Perfect score: 370

Sequence: 1 NAKRPPSAFFLCSEYRPK.....QPYEKKAALKKEKYEKDIAA 69

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS5/ptodata/2/pubpaa/US08\_NEW\_PUB\_PEP.\*
- 2: /SIDSS5/ptodata/2/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 3: /SIDSS5/ptodata/2/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 4: /SIDSS5/ptodata/2/pubpaa/US09\_NEW\_PUB\_PEP.\*
- 5: /SIDSS5/ptodata/2/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 6: /SIDSS5/ptodata/2/pubpaa/US11\_NEW\_PUB\_PEP.\*
- 7: /SIDSS5/ptodata/2/pubpaa/US12\_NEW\_PUB\_PEP.\*
- 8: /SIDSS5/ptodata/2/pubpaa/US13\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	69	7	US-11-186-422-14
2	370	100.0	215	6	US-10-821-234-1443
3	370	100.0	215	7	US-11-186-422-11
4	370	100.0	215	7	US-11-186-422-12
5	317	85.7	879	7	US-11-169-041-192
6	279	75.4	169	6	US-10-821-234-1234
7	168.5	45.5	139	7	US-11-096-568A-26884
8	168.5	45.5	187	7	US-11-096-568A-26883
9	165	44.6	92	7	US-11-087-099-9838
10	164.5	44.5	141	7	US-11-087-099-3073
11	163	44.1	93	7	US-11-087-099-9518
12	163	44.1	93	7	US-11-087-099-9518
13	162.5	43.9	149	7	US-11-087-099-3510
14	162.5	43.9	149	7	US-11-172-740-1571
15	159.5	43.1	141	7	US-11-087-099-9185
16	157.5	42.6	139	7	US-11-096-568A-13611
17	157.5	42.6	142	7	US-11-087-099-4976
18	156	42.2	99	7	US-11-087-099-2564
19	156	42.2	99	7	US-11-087-099-10060
20	154.5	41.8	124	7	US-11-096-568A-9681
21	154.5	41.8	162	7	US-11-096-568A-9680
22	153	41.4	187	7	US-11-096-568A-32735
23	153	41.4	241	7	US-11-096-568A-32734
24	153	41.4	257	7	US-11-096-568A-32733
25	151.5	40.9	160	7	US-11-087-099-1105

26	151	40.8	446	7	US-11-087-099-370	Sequence 370, App
27	150.5	40.7	127	7	US-11-096-568A-15615	Sequence 15615, A
28	150.5	40.7	154	7	US-11-096-568A-15614	Sequence 15614, A
29	149.5	40.4	146	7	US-11-172-740-1569	Sequence 1569, Ap
30	148.5	40.1	106	7	US-11-087-099-7075	Sequence 7075, Ap
31	148.5	40.1	152	7	US-11-087-099-313	Sequence 313, App
32	148.5	40.1	152	7	US-11-172-740-1565	Sequence 1565, Ap
33	148.5	40.1	152	7	US-11-172-740-1566	Sequence 1566, Ap
34	145	39.2	108	7	US-11-087-099-6594	Sequence 6594, Ap
35	144.5	39.1	145	7	US-11-172-740-1572	Sequence 1572, Ap
36	143	38.6	473	6	US-10-542-161-1	Sequence 1, Appli
37	142	38.4	310	7	US-11-087-099-4210	Sequence 4210, Ap
38	142	38.4	487	7	US-11-124-368A-308	Sequence 308, App
39	142	38.4	487	7	US-11-124-368A-309	Sequence 309, App
40	142	38.4	526	7	US-11-124-368A-310	Sequence 310, App
41	141.5	38.2	165	7	US-11-096-568A-21033	Sequence 21033, A
42	141.5	38.2	212	7	US-11-096-568A-21032	Sequence 21032, A
43	141.5	38.2	234	7	US-11-096-568A-21031	Sequence 21031, A
44	140.5	38.0	154	7	US-11-087-099-2474	Sequence 2474, Ap
45	140.5	38.0	154	7	US-11-172-740-1570	Sequence 1570, Ap

## ALIGNMENTS

### RESULT 1

US-11-186-422-14  
; Sequence 14, Application US/11186422  
; Publication No. US20060057679A1  
; GENERAL INFORMATION:  
; APPLICANT: Critical Therapeutics, Inc.  
; APPLICANT: O'Keeffe, Theresa  
; APPLICANT: Luciano, Peter  
; APPLICANT: Qin, Shixin  
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES  
; FILE REFERENCE: 3258.1021-003  
; CURRENT APPLICATION NUMBER: US/11/186.422  
; PRIOR FILING DATE: 2005-07-20  
; PRIOR APPLICATION NUMBER: 60/589,678  
; PRIOR FILING DATE: 2004-07-20  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 69  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-186-422-14

Query Match 100.0%; Score 370; DB 7; Length 69;  
Best Local Similarity 100.0%; Pred. No. 1.6e-37;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAKRPPSAFFLCSEYRPKIKGEHPGLSGDVAKKLGMNNTAADKOPYEKKAALK 60  
|||||  
DB 1 NAKRPPSAFFLCSEYRPKIKGEHPGLSGDVAKKLGMNNTAADKOPYEKKAALK 60  
|||||

QY 61 EKYEKDIAA 69  
|||||  
DB 61 EKYEKDIAA 69

### RESULT 2

US-10-821-234-1443  
; Sequence 1443, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234

```
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1443
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1443

Query Match      100.0%; Score 370; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 60
Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 152

QY 61 EYKEDIAA 69
Db 153 EYKEDIAA 161

RESULT 3
US-11-186-422-11
; Sequence 11, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-11

Query Match      100.0%; Score 370; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 60
Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 152

QY 61 EYKEDIAA 69
Db 153 EYKEDIAA 161

RESULT 4
US-11-186-422-12
; Sequence 12, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
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; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-186-422-12

Query Match      100.0%; Score 370; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 60
Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 152

QY 61 EYKEDIAA 69
Db 153 EYKEDIAA 161

RESULT 5
US-11-169-041-192
; Sequence 192, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 192
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-192

Query Match      85.7%; Score 317; DB 7; Length 879;
Best Local Similarity 88.4%; Pred. No. 7.4e-30;
Matches 61; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 60
Db 767 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAK 826

QY 61 EYKEDIAA 69
Db 827 EYKEDIAA 835

RESULT 6
US-10-821-234-1234
; Sequence 1234, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
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; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes version 1.0
; SEQ ID NO 1234
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(169)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1234

Query Match          75.4%; Score 279; DB 6; Length 169;
Best Local Similarity 75.0%; Pred. No. 3.7e-26;
Matches 51; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 NAPRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 60
    |||||
Db 80 NAPRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 60
    |||||

QY 61 EYKEDIA 68
    |||||
Db 140 EYKEDIA 147

RESULT 7
US-11-096-568A-26884
; Sequence 26884, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26884
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(139)
; OTHER INFORMATION: Ceres Seq. ID no. 13627626
US-11-096-568A-26884

Query Match          45.5%; Score 168.5; DB 7; Length 139;
Best Local Similarity 48.4%; Pred. No. 5e-13;
Matches 31; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 3 PKRPPSAFFLFCSEYRPKIKGEHPG-LSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 61
    |||||
Db 34 PKRPPSAFFVFMSEFRQYQAOHPGNKSVAAVSKAAGEKWRSMSEQKQPYVDQAGKKQ 93
    |||||

QY 62 KYEK 65
    |||||
Db 94 DYK 97

RESULT 8
US-11-096-568A-26883
; Sequence 26883, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
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; SEQ ID NO 26883
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(187)
; OTHER INFORMATION: Ceres Seq. ID no. 13627625
US-11-096-568A-26883

Query Match          45.5%; Score 168.5; DB 7; Length 187;
Best Local Similarity 48.4%; Pred. No. 7.1e-13;
Matches 31; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 3 PKRPPSAFFLFCSEYRPKIKGEHPG-LSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 61
    |||||
Db 82 PKRPPSAFFVFMSEFRQYQAOHPGNKSVAAVSKAAGEKWRSMSEQKQPYVDQAGKKQ 141
    |||||

QY 62 KYEK 65
    |||||
Db 142 DYK 145

RESULT 9
US-11-087-099-8838
; Sequence 8838, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8838
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Candida albicans
US-11-087-099-8838

Query Match          44.6%; Score 165; DB 7; Length 92;
Best Local Similarity 47.1%; Pred. No. 8e-13;
Matches 32; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

QY 1 NAPRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALK 60
    |||||
Db 17 DAPKRSLSAYMFPANENRDIVRAENPGISFGQVGLGKWKALNSEDKL PYENKAEADK 76
    |||||

QY 61 EYKEDIA 68
    |||||
Db 77 KRYEKEKA 84

RESULT 10
US-11-087-099-3073
; Sequence 3073, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3073
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Canavalia gladiata
US-11-087-099-3073

Query Match          44.5%; Score 164.5; DB 7; Length 141;
Best Local Similarity 47.1%; Pred. No. 1.5e-12;
Matches 33; Conservative 12; Mismatches 24; Indels 1; Gaps 1;
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; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants with increased biomass
US-11-172-740-1571

```

```

Query Match 43.9%; Score 162.5; DB 7; Length 149;
Best Local Similarity 44.3%; Pred. No. 2.8e-12;
Matches 31; Conservative 14; Mismatches 24; Indels 1; Gaps 1;

Qy 1 NAKRPPSAFLFCSEYRPKIKGEHP-GLSIGDVAKLGEWMNNTAADDKOPYEKKAAKL 59
Db 43 NAKRPPSAFLFCSEYRPKIKGEHP-GLSIGDVAKLGEWMNNTAADDKOPYEKKAAKL 102

Qy 60 KEYEKDIAA 69
Db 103 KEEYEITLQA 112

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RESULT 15
US-11-087-099-9185
; Sequence 9185, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9185
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-9185

```

```

Query Match 43.1%; Score 159.5; DB 7; Length 141;
Best Local Similarity 44.3%; Pred. No. 6.1e-12;
Matches 31; Conservative 13; Mismatches 25; Indels 1; Gaps 1;

Qy 1 NAKRPPSAFLFCSEYRPKIKGEHP-GLSIGDVAKLGEWMNNTAADDKOPYEKKAAKL 59
Db 34 NAKRPPSAFLFCSEYRPKIKGEHP-GLSIGDVAKLGEWMNNTAADDKOPYEKKAAKL 93

Qy 60 KEYEKDIAA 69
Db 94 KAEYQKQMDA 103

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Search completed: April 6, 2006, 10:33:31  
Job time : 9.625 secs

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CC naturally occurring HMG A box inhibits the release of a pro-inflammatory  
CC cytokine from a vertebrate cell. The methods and compositions of the  
CC invention are useful for inhibiting a condition characterised by  
CC activation of an inflammatory cytokine cascade such as endotoxic shock,  
CC rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's  
CC disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,  
CC sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,  
CC filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,  
CC myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout,  
CC cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host  
CC disease, diabetes and Hodgkin's disease. The invention is useful in gene  
CC therapy. The present sequence is human HMGI (also termed as HMGB1) B box  
CC fragment

XX Sequence 20 AA;

Query Match 100.0%; Score 110; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.5e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20  
|||||  
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 2  
ADO25940  
ID ADO25940 standard; peptide; 20 AA.

XX ADO25940;

XX 26-AUG-2004 (first entry)

DE Tumour necrosis factor stimulating peptide.

XX cytostatic; gene therapy; vaccine; pharmaceutical composition;  
KW HMGB B box; high mobility group; immune response; immunostimulation;  
KW cancer; human; high mobility group box 1; HMGI; cytokine activity;  
KW TNF stimulating; tumour necrosis factor stimulating.

XX Synthetic.

XX WO2004046338-A2.

XX 03-JUN-2004.

XX 19-NOV-2003; 2003WO-US036975.

XX 20-NOV-2002; 2002US-0427848P.

XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.

XX Tracey KJ;

XX WPI; 2004-420625/39.

XX New pharmaceutical composition comprises a polypeptide comprising an HMGB  
PT B box or its functional variant, useful for stimulating or increasing an  
PT immune response in an individual or for treating cancer in an individual.

PS Example 4; SEQ ID NO 23; 68pp; English.

XX The invention describes a pharmaceutical composition comprising a  
CC polypeptide comprising an HMGB (high mobility group box) B box or its  
CC functional variant to treat a disease or condition by increasing an  
CC immune response in an individual administered with the pharmaceutical  
CC composition. Also described are: an antibody attached to a polypeptide  
CC comprising an HMGB B box or its functional variant; stimulating or  
CC increasing an immune response in an individual in need of  
CC immunostimulation; and treating cancer in an individual. The composition  
CC is useful for stimulating or increasing an immune response in an  
CC individual in need of immunostimulation or for treating cancer in an  
CC individual. This is the amino acid sequence of tumour necrosis factor

CC (TNF) stimulating peptide based on amino acids 1-20 of the human high  
CC mobility group box 1 (HMGI) protein.

XX Sequence 20 AA;

Query Match 100.0%; Score 110; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.5e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20  
|||||  
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 3  
ADO71499

ID ADO71499 standard; peptide; 20 AA.

XX ADO71499;

XX 26-AUG-2004 (first entry)

XX Human high mobility group box 1 (HMGB1) B box protein active fragment #2.

XX Human; high mobility group box 1 B box; HMGB1 B box; HMGB A box;  
KW HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation;  
KW inflammatory cytokine cascade; sepsis; allograft rejection;  
KW rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;  
KW chronic obstructive pulmonary disease; psoriasis; pancreatitis;  
KW peritonitis; burn; myocardial ischaemia; organic ischaemia;  
KW reperfusion ischaemia; Behcet's disease; graft-versus-host disease;  
KW Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.

XX Homo sapiens.

XX WO2004046345-A2.

XX 03-JUN-2004.

XX 20-NOV-2003; 2003WO-US037507.

XX 20-NOV-2002; 2002US-0427841P.

XX 20-NOV-2002; 2002US-0427846P.

XX (CRIT-) CRITICAL THERAPEUTICS INC.

XX Newman W, O'keefe TL;

XX WPI; 2004-420628/39.

XX New high mobility group box proteins, useful in treating obesity, sepsis,  
PT rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,  
PT Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.

PS Claim 33; SEQ ID NO 23; 113pp; English.

XX The invention relates to a polypeptide comprising a high mobility group  
CC box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of  
CC a proinflammatory cytokine from a cell treated with an HMGB protein. The  
CC invention also relates to a purified preparation of antibodies that  
CC specifically bind to the HMGB B box but do not specifically bind to non-B  
CC box epitopes of HMGB, where the antibodies can inhibit release of a  
CC proinflammatory cytokine from a cell treated with HMGB, a method of  
CC affecting weight loss or treating obesity in a patient, a method of  
CC determining whether a compound inhibits inflammation, a pharmaceutical  
CC composition comprising an HMGB protein or an antibody that binds to the  
CC protein, an agent that inhibits TNF biological activity and a method of  
CC treating a condition in a patient characterised by activation of an  
CC inflammatory cytokine cascade. Effecting weight loss or treating obesity  
CC in a patient comprises administering to the patient an amount of the  
CC polypeptide. The polypeptide, antibodies, composition and methods are  
CC useful in treating obesity and conditions characterised by activation of  
CC an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,



CC rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,  
 CC chronic obstructive pulmonary disease, psoriasis, pancreatitis,  
 CC peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion  
 CC ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,  
 CC ulcerative colitis, multiple sclerosis or cachexia. This sequence  
 CC represents a human HMGB1 B box polypeptide active fragment of the  
 CC invention.  
 CC  
 XX  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 110; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
 |||||  
 DB 1 FKDPNAPKRLPSAFFLFCSE 20  
 |||||

RESULT 4  
 AAE35868  
 ID AAE35868 standard; protein; 74 AA.  
 XX  
 AC AAE35868;  
 XX  
 DT 17-JUN-2003 (first entry)  
 XX  
 DE Human HMGB1 protein mutant #2.  
 XX  
 KW Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma;  
 KW inflammatory cytokine; endotoxin shock; rheumatoid arthritis; hepatitis;  
 KW appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis;  
 KW allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis;  
 KW emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis;  
 KW Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes;  
 KW Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease;  
 KW anoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis;  
 KW gene therapy; human immunodeficiency virus; HMGB1 protein; mutant;  
 KW mutuin.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200292004-A2.  
 XX  
 PD 21-NOV-2002.  
 XX  
 PF 15-MAY-2002; 2002WO-US015329.  
 XX  
 PR 15-MAY-2001; 2001US-0291034P.  
 XX  
 PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (UYPI-) UNIV PITTSBURGH.  
 XX  
 PI Tracey KJ, Yang H, Warren HS, Fink MP;  
 XX  
 DR WPI; 2003-120594/11.  
 XX  
 PT New isolated polypeptide having a vertebrate HMG A box, useful for  
 PT inhibiting a condition associated with an activated inflammatory cytokine  
 PT cascade, e.g. endotoxin shock, myocardial infarction, asthma, HIV  
 PT infection, malaria and diabetes.  
 XX  
 PS Example 1; Page 37; 82pp; English.  
 XX  
 CC The invention relates to high mobility group (HMG) protein comprising DNA  
 CC binding motifs termed HMG A box and HMG B box. HMG A box or a non-  
 CC naturally occurring HMG A box inhibits the release of a pro-inflammatory  
 CC cytokine from a vertebrate cell. The methods and compositions of the  
 CC invention are useful for inhibiting a condition characterised by  
 CC activation of an inflammatory cytokine cascade such as endotoxin shock,  
 CC rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's

CC disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,  
 CC sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,  
 CC filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,  
 CC myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout,  
 CC cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host  
 CC disease, diabetes and Hodgkin's disease. The invention is useful in gene  
 CC therapy. The present sequence is human HMGB1 (also termed as HMGB1)  
 CC protein (B box) mutant  
 XX  
 SQ Sequence 74 AA;

Query Match 100.0%; Score 110; DB 6; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
 |||||  
 DB 1 FKDPNAPKRLPSAFFLFCSE 20  
 |||||

RESULT 5  
 ADO25937  
 ID ADO25937 standard; protein; 74 AA.  
 XX  
 AC ADO25937;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Human high mobility group box 1 B-box mutant.  
 XX  
 KW Cytostatic; gene therapy; vaccine; pharmaceutical composition;  
 KW HMG B box; high mobility group; immune response; immunostimulation;  
 KW cancer; human; high mobility group box 1; HMGB1; cytokine activity;  
 KW mutant; mutuin.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO2004046338-A2.  
 XX  
 PD 03-JUN-2004.  
 XX  
 PF 19-NOV-2003; 2003WO-US036975.  
 XX  
 PR 20-NOV-2002; 2002US-0427848P.  
 XX  
 PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 XX  
 PI Tracey KJ;  
 XX  
 DR WPI; 2004-420625/39.  
 XX  
 PT New pharmaceutical composition comprises a polypeptide comprising an HMGB  
 PT B box or its functional variant, useful for stimulating or increasing an  
 PT immune response in an individual or for treating cancer in an individual.  
 XX  
 PS Example 1; SEQ ID NO 20; 68pp; English.  
 XX  
 CC The invention describes a pharmaceutical composition comprising a  
 CC polypeptide comprising an HMGB (high mobility group box) B box or its  
 CC functional variant to treat a disease or condition by increasing an  
 CC immune response in an individual administered with the pharmaceutical  
 CC composition. Also described are: an antibody attached to a polypeptide  
 CC comprising an HMGB B box or its functional variant; stimulating or  
 CC increasing an immune response in an individual in need of  
 CC immunostimulation; and treating cancer in an individual. The composition  
 CC is useful for stimulating or increasing an immune response in an  
 CC individual in need of immunostimulation or for treating cancer in an  
 CC individual. This is the amino acid sequence of a human high mobility  
 CC group box 1 (HMGB1) B box mutant.  
 XX  
 SQ Sequence 74 AA;

```

Query Match      100.0%; Score 110; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 8.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 6
ADO25958
ID ADO25958 standard; peptide; 74 AA.
XX
AC ADO25958;
XX
DE 26-AUG-2004 (first entry)
XX
DE High mobility group box 1 B box fragment seqid 41.
XX
KW cytotatic; gene therapy; vaccine; pharmaceutical composition;
KW HMGB B box; high mobility group; immune response; immunostimulation;
KW cancer; human; high mobility group box 1; HMGB1; cytokine activity; B box.
XX
OS Homo sapiens.
XX
PN WO2004046338-A2.
XX
PD 03-JUN-2004.
XX
PF 19-NOV-2003; 2003WO-US036975.
XX
PR 20-NOV-2002; 2002US-0427848P.
XX
PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI Tracey KJ;
XX
DR WPI; 2004-420625/39.
XX
PT New pharmaceutical composition comprises a polypeptide comprising an HMGB
PT B box or its functional variant, useful for stimulating or increasing an
PT immune response in an individual or for treating cancer in an individual.
XX
PS Disclosure; SEQ ID NO 41; 68pp; English.
XX
CC The invention describes a pharmaceutical composition comprising a
CC polypeptide comprising an HMGB (high mobility group box) B box or its
CC functional variant to treat a disease or condition by increasing an
CC immune response in an individual administered with the pharmaceutical
CC composition. Also described are: an antibody attached to a polypeptide
CC comprising an HMGB B box or its functional variant; stimulating or
CC increasing an immune response in an individual in need of
CC immunostimulation; and treating cancer in an individual. The composition
CC is useful for stimulating or increasing an immune response in an
CC individual in need of immunostimulation or for treating cancer in an
CC individual. This is the amino acid sequence of human high mobility group
CC box 1 (HMGB) B box biologically active fragment.
XX
SQ Sequence 74 AA;

Query Match      100.0%; Score 110; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 8.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 7
ADO71496
ID ADO71496 standard; protein; 74 AA.
XX
AC ADO71496;
XX
DE 26-AUG-2004 (first entry)
XX
DE Human high mobility group box 1 (HMGB1) mutant protein #2.
XX
KW Human; high mobility group box 1; HMGB1; HMGB; HMGB A box; HMGB B box;
KW proinflammatory cytokine; weight loss; obesity; inflammation;
KW inflammatory cytokine cascade; sepsis; allograft rejection;
KW rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;
KW chronic obstructive pulmonary disease; psoriasis; pancreatitis;
KW peritonitis; burn; myocardial ischaemia; organic ischaemia;
KW reperfusion ischaemia; Behcet's disease; graft-versus-host disease;
KW Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004046345-A2.
XX
PD 03-JUN-2004.
XX
PF 20-NOV-2003; 2003WO-US037507.
XX
PR 20-NOV-2002; 2002US-0427841P.
XX
PR 20-NOV-2002; 2002US-0427846P.
XX
PA (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI Newman W, O'Keefe TL;
XX
DR WPI; 2004-420628/39.
XX
PT New high mobility group box proteins, useful in treating obesity, sepsis,
PT rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,
PT Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
XX
PS Example 1; SEQ ID NO 20; 113pp; English.
XX
CC The invention relates to a polypeptide comprising a high mobility group
CC box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of
CC a proinflammatory cytokine from a cell treated with an HMGB protein. The
CC invention also relates to a purified preparation of antibodies that
CC specifically bind to the HMGB B box but do not specifically bind to non-B
CC epitopes of HMGB, where the antibodies can inhibit release of a
CC proinflammatory cytokine from a cell treated with HMGB, a method for
CC effecting weight loss or treating obesity in a patient, a method of
CC determining whether a compound inhibits inflammation, a pharmaceutical
CC composition comprising an HMGB protein or an antibody that binds to the
CC protein, an agent that inhibits TNF biological activity and a method of
CC treating a condition in a patient characterised by activation of an
CC inflammatory cytokine cascade. Effecting weight loss or treating obesity
CC in a patient comprises administering to the patient an amount of the
CC polypeptide. The polypeptide, antibodies, composition and methods are
CC useful in treating obesity and conditions characterised by activation of
CC an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
CC rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,
CC chronic obstructive pulmonary disease, psoriasis, pancreatitis,
CC peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion
CC ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,
CC ulcerative colitis, multiple sclerosis or cachexia. This sequence
CC represents a human HMGB1 mutant polypeptide of the invention.
XX
SQ Sequence 74 AA;

Query Match      100.0%; Score 110; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 8.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
Db 1 FKDPNAPKRLPSAFFLFCSE 20

```

RESULT 8  
 ADO71529 ID ADO71529 standard; protein; 74 AA.  
 AC ADO71529;  
 XX  
 XX  
 DT 26-AUG-2004 (first entry)  
 DE Human high mobility group box (HMGB) B box protein #3.  
 XX  
 XX Human; high mobility group box B box; HMGB; HMGB A box; HMGB B box;  
 KW proinflammatory cytokine; weight loss; obesity; inflammation;  
 KW inflammatory cytokine cascade; sepsis; allograft rejection;  
 KW rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;  
 KW chronic obstructive pulmonary disease; psoriasis; pancreatitis;  
 KW peritonitis; burn; myocardial ischaemia; organic ischaemia;  
 KW reperfusion ischaemia; Behcet's disease; graft-versus-host disease;  
 KW Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2004046345-A2.  
 PN  
 XX  
 PD 03-JUN-2004.  
 XX  
 PF 20-NOV-2003; 2003WO-US037507.  
 XX  
 PF 20-NOV-2002; 2002US-0427841P.  
 PR 20-NOV-2002; 2002US-0427846P.  
 XX  
 XX (CRIT-) CRITICAL THERAPEUTICS INC.  
 PA  
 XX Newman W, O'keefe TL;  
 XX WPI; 2004-420628/39.  
 DR  
 XX  
 XX New high mobility group box proteins, useful in treating obesity, sepsis,  
 PT rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischaemia,  
 PT Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.  
 XX  
 PS Disclosure; SEQ ID NO 53; 113pp; English.  
 XX  
 CC The invention relates to a polypeptide comprising a high mobility group  
 CC box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of  
 CC a proinflammatory cytokine from a cell treated with an HMGB protein. The  
 CC invention also relates to a purified preparation of antibodies that  
 CC specifically bind to the HMGB B box but do not specifically bind to non-B  
 CC box epitopes of HMGB, where the antibodies can inhibit release of a  
 CC proinflammatory cytokine from a cell treated with HMGB, a method for  
 CC effecting weight loss or treating obesity in a patient, a method of  
 CC determining whether a compound inhibits inflammation, a pharmaceutical  
 CC composition comprising an HMGB protein or an antibody that binds to the  
 CC protein, an agent that inhibits TNF biological activity and a method of  
 CC treating a condition in a patient characterised by activation of an  
 CC inflammatory cytokine cascade. Effecting weight loss or treating obesity  
 CC in a patient comprises administering to the patient an amount of the  
 CC polypeptide. The polypeptide, antibodies, composition and methods are  
 CC useful in treating obesity and conditions characterised by activation of  
 CC an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,  
 CC rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,  
 CC chronic obstructive pulmonary disease, psoriasis, pancreatitis,  
 CC peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion  
 CC ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,  
 CC ulcerative colitis, multiple sclerosis or cachexia. This sequence  
 CC represents a human HMGB B box polypeptide of the invention.  
 XX  
 SQ Sequence 74 AA;  
 Query Match 100.0%; Score 110; DB 8; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLPCSE 20  
 DB |||||  
 1 FKDPNAPKRLPSAFFLPCSE 20  
 RESULT 9  
 ADY85364  
 ID ADY85364 standard; protein; 74 AA.  
 XX AC  
 XX ADY85364;  
 XX  
 DT 02-JUN-2005 (first entry)  
 DE Human high mobility group box protein HMGLL10 B box.  
 XX  
 XX High mobility group box; HMGLL10; immune disorder; infection;  
 KW immunosuppressive; autoimmune disease; allergy; anti-allergic;  
 KW ulcerative colitis; anti-inflammatory; antiulcer; gastrointestinal-gen.;  
 KW Crohn's disease; inflammation; asthma; antiasthmatic;  
 KW rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis;  
 KW antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.  
 XX  
 OS Unidentified.  
 XX  
 XX WO2005025604-A2.  
 PN  
 XX  
 PD 24-MAR-2005.  
 XX  
 PF 10-SEP-2004; 2004WO-US029540.  
 XX  
 PF 10-SEP-2003; 2003US-0502349P.  
 PR  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 XX Warren HS, Tracey KJ;  
 XX WPI; 2005-233421/24.  
 DR  
 XX  
 XX Treating an immune pathology in an individual comprises administering an  
 PT amount of a high mobility group box (HMGB) polypeptide comprising a  
 PT vertebrate or a non-naturally occurring HMGB A or B box, or its  
 PT immunosuppressive fragment.  
 XX  
 PS Disclosure; SEQ ID NO 39; 57pp; English.  
 XX  
 CC The invention is based on the discovery that high mobility group box  
 CC protein 1 (HMGB1, also known as high mobility group-1 or HMGL1), when  
 CC administered with an antigen, diminishes the antibody response to the  
 CC administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B  
 CC boxes. A claimed method of treating an immune pathology in an individual  
 CC comprises administering a HMGB polypeptide comprising a vertebrate HMGB A  
 CC box, a non-naturally-occurring HMGB A box, or an immunosuppressive  
 CC fragment of the vertebrate or non-natural HMGB A box. The immune  
 CC pathology is induced by the administration of a non-human antigen, non-  
 CC self material (e.g. a cell or tissue such as bone marrow cells) or  
 CC adjuvant to the individual, by the transplantation of an organ into the  
 CC individual, or by infection from a microorganism. Claimed methods of  
 CC protecting a subject against an immune pathology, inhibiting an immune  
 CC pathology in an individual or decreasing an immune response to an  
 CC administered non-human antigen comprise administering a HMGB polypeptide  
 CC comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box,  
 CC or an immunosuppressive fragment of the vertebrate or non-natural A box.  
 CC A claimed method of treating an autoimmune disorder in an individual  
 CC comprises administering a HMGB polypeptide comprising a vertebrate HMGB A  
 CC box, a non-naturally-occurring HMGB A box, or an immunosuppressive  
 CC fragment of these, and a vertebrate or non-naturally-occurring HMGB B  
 CC box. The HMGB polypeptide is preferably a HMGB1 peptide and may be  
 CC truncated at the C-terminus. The autoimmune disease is allergy,  
 CC ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis,  
 CC psoriasis or systemic lupus erythematosus (all claimed). The present  
 CC sequence is that of the B box of human HMGLL10, a HMGB protein.

```

XX SQ Sequence 74 AA;
Query Match 100.0%; Score 110; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 8.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
   ||||| ||||| ||||| |||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 10
ADY85333
ID ADY85333 standard; protein; 74 AA.
XX
AC ADY85333;
XX
DT 02-JUN-2005 (first entry)
XX
DE High mobility group box protein HMGB1 B box mutant.
XX
DE High mobility group box; HMGB1; immune disorder; infection;
XX immunosuppressive; autoimmune disease; allergy; anti-allergic;
XX ulcerative colitis; anti-inflammatory; antiulcer; gastrointestinal-gen.;
XX Crohns disease; inflammation; asthma; antiasthmatic;
XX rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis;
XX antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer;
XX mitein.
XX
OS Homo sapiens.
OS Mus sp.
OS Rattus sp.
OS Synthetic.
XX
XX WO2005025604-A2.
XX
XX 24-MAR-2005.
XX
PD 10-SEP-2004; 2004WO-US029540.
XX
PF 10-SEP-2003; 2003US-0502349P.
XX
PR (GEHO ) GEN HOSPITAL CORP.
PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
XX Warren HS, Tracey KJ;
PI WPI; 2005-233421/24.
XX
XX Treating an immune pathology in an individual comprises administering an
XX amount of a high mobility group box (HMGB) polypeptide comprising a
XX vertebrate or a non-naturally occurring HMGB A or B box, or its
XX immunosuppressive fragment.
XX
XX Example 1; SEQ ID NO 8; 57pp; English.
XX
XX The invention is based on the discovery that high mobility group box
XX protein 1 (HMGB1, also known as high mobility group-1 or HMGI), when
XX administered with an antigen, diminishes the antibody response to the
XX administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B
XX boxes. A claimed method of treating an immune pathology in an individual
XX comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
XX box, a non-naturally-occurring HMGB A box, or an immunosuppressive
XX fragment of the vertebrate or non-natural HMGB A box. The immune
XX pathology is induced by the administration of a non-human antigen, non-
XX self material (e.g. a cell or tissue such as bone marrow cells) or
XX adjuvant to the individual, by the transplantation of an organ into the
XX individual, or by infection from a microorganism. Claimed methods of
XX protecting a subject against an immune pathology, inhibiting an immune
XX pathology in an individual or decreasing an immune response to an
XX administered non-human antigen comprise administering a HMGB polypeptide
XX comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box,
or an immunosuppressive fragment of the vertebrate or non-natural A box.
A claimed method of treating an autoimmune disorder in an individual
comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
box, a non-naturally-occurring HMGB A box, or an immunosuppressive
fragment of these, and a vertebrate or non-naturally-occurring HMGB B
box. The HMGB polypeptide is preferably a HMGB1 peptide and may be
truncated at the C-terminus. The autoimmune disease is allergy,
psoriasis or systemic lupus erythematosus (all claimed). The present
sequence is that of a mutated B box of human, mouse and rat HMGB1
proteins ADY85326-ADY85327, which was produced in an example from the
invention.
XX
XX SQ Sequence 74 AA;
Query Match 100.0%; Score 110; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 8.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
   ||||| ||||| ||||| |||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 11
ADY85080
ID ADY85080 standard; protein; 74 AA.
XX
AC ADY85080;
XX
XX 16-JUN-2005 (first entry)
XX
DE Human HMGB1 A box.
XX
DE High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
XX sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
XX antiarthritic; asthma; antiasthmatic; lupus erythematosus;
XX anti-inflammatory; inflammation; dermatological;
XX respiratory distress syndrome; respiratory-gen.; psoriasis;
XX antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
XX peritonitis; burns; vulnery; ischemia; vasotropic; Behcets disease;
XX graft versus host disease; inflammatory bowel disease;
XX gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
XX anabolic; infection; musculoskeletal disease; immune disorder.
XX
XX Homo sapiens.
XX Mus sp.
XX Rattus sp.
XX
XX WO2005026209-A2.
XX
XX 24-MAR-2005.
XX
PF 10-SEP-2004; 2004WO-US029527.
XX
XX 11-SEP-2003; 2003US-0502568P.
XX
XX (CRIT-) CRITICAL THERAPEUTICS INC.
XX
XX Newman W, Qin S, Okeefe T, Obar R;
XX WPI; 2005-233483/24.
XX
XX New antibody or its antigen-binding fragment specific to a vertebrate
XX high mobility group box (HMGB) A box that inhibits release of a
XX proinflammatory cytokine from a cell treated with HMGB protein, useful
XX for treating, e.g. sepsis.
XX
XX Disclosure; SEQ ID NO 2; 123pp; English.
XX
XX The invention provides antibodies, or their antigen-binding fragments, to
XX that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
XX methods of detecting and/or identifying an agent that binds to an HMGB

```

CC polypeptide, methods of treating a condition in a subject characterized  
 CC by activation of an inflammatory cytokine cascade, and methods of  
 CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-  
 CC binding fragment) binds to a vertebrate HMGB A box but does not  
 CC specifically bind to non-A box epitopes of HMGB, and inhibits release of  
 CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB  
 CC protein. A method of treating a condition characterized by activation of  
 CC an inflammatory cytokine cascade comprises administering an antibody of  
 CC the invention, or its antigen-binding fragment. The condition is selected  
 CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult  
 CC respiratory distress syndrome, chronic obstructive pulmonary disease,  
 CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,  
 CC graft versus host disease, inflammatory bowel disease, multiple sclerosis  
 CC and cachexia, especially sepsis, arthritis, or lupus. The present  
 CC sequence is that of the A box of human HMGB1 ADY85012. An identical  
 CC sequence is also found in rat and mouse HMGB1.

XX SQ Sequence 74 AA;

Query Match 100.0%; Score 110; DB 9; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLCSE 20  
 |||||  
 Db 1 FKDPNAPKRLPSAFFLCSE 20

RESULT 12  
 ADY85014

ID ADY85014 standard; protein; 74 AA.

XX AC ADY85014;

XX DT 16-JUN-2005 (first entry)

XX DE Human HMGB1 A box.

XX High mobility group box; HMGB1; monoclonal antibody; antibody therapy;  
 KW sepsis; antibacterial immunosuppressive; graft rejection; arthritis;  
 KW antiarthritic; asthma; antiasthmatic; lupus erythematosus;  
 KW antiinflammatory; inflammation; dermatological;  
 KW respiratory distress syndrome; respiratory-gen.; psoriasis;  
 KW asthenoasthmatic; chronic obstructive pulmonary disease; pancreatitis;  
 KW peritonitis; burns; vulnery; ischemia; vasotropic; Behcet's disease;  
 KW graft versus host disease; inflammatory bowel disease;  
 KW gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;  
 KW anabolic; infection; musculoskeletal disease; immune disorder.

XX OS Homo sapiens.

XX OS Mus sp.

XX OS Rattus sp.

XX PN WO2005026209-A2.

XX XX 24-MAR-2005.

XX PF 10-SEP-2004; 2004WO-US029527.

XX PR 11-SEP-2003; 2003US-0502568P.

XX XX (CRIT-) CRITICAL THERAPEUTICS INC.

XX PI Newman W, Qin S, Okeefe T, Obar R;

XX DR WPI; 2005-233483/24.

XX New antibody or its antigen-binding fragment specific to a vertebrate  
 PT high mobility group box (HMGB) A box that inhibits release of a  
 PT proinflammatory cytokine from a cell treated with HMGB protein, useful  
 PT for treating, e.g. sepsis.

XX PS Disclosure; SEQ ID NO 2; 123pp; English.

XX The invention provides antibodies, or their antigen-binding fragments,  
 CC that bind to a vertebrate high mobility group box (HMGB) polypeptide, to  
 CC methods of detecting and/or identifying an agent that binds to an HMGB  
 CC polypeptide, methods of treating a condition in a subject characterized  
 CC by activation of an inflammatory cytokine cascade, and methods of  
 CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-  
 CC binding fragment) binds to a vertebrate HMGB A box but does not  
 CC specifically bind to non-A box epitopes of HMGB, and inhibits release of  
 CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB  
 CC protein. A method of treating a condition characterized by activation of  
 CC an inflammatory cytokine cascade comprises administering an antibody of  
 CC the invention, or its antigen-binding fragment. The condition is selected  
 CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult  
 CC respiratory distress syndrome, chronic obstructive pulmonary disease,  
 CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,  
 CC graft versus host disease, inflammatory bowel disease, multiple sclerosis  
 CC and cachexia, especially sepsis, arthritis, or lupus. The present  
 CC sequence is that of the A box of human HMGB1 ADY85012. An identical  
 CC sequence is also found in rat and mouse HMGB1.

XX SQ Sequence 74 AA;

Query Match 100.0%; Score 110; DB 9; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLCSE 20  
 |||||  
 Db 1 FKDPNAPKRLPSAFFLCSE 20

RESULT 13

AAE35867

ID AAE35867 standard; protein; 182 AA.

XX AC AAE35867;

XX DT 17-JUN-2003 (first entry)

XX DE Human HMGB1 protein mutant #1.

XX Human; high mobility group; HMGB protein; HMGB A box; HMGB B box; asthma;  
 KW inflammatory cytokine; endotoxin shock; rheumatoid arthritis; hepatitis;  
 KW appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis;  
 KW allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis;  
 KW emphysema; HIV infection; candidiasis; malaria; filariasis; myocardiitis;  
 KW Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes;  
 KW Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease;  
 KW amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis;  
 KW gene therapy; human immunodeficiency virus; HMGB1 protein; mutant;  
 KW mutein.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200292004-A2.

XX PD 21-NOV-2002.

XX PF 15-MAY-2002; 2002WO-US015329.

XX PR 15-MAY-2001; 2001US-0291034P.

XX XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PA (UYPI-) UNIV PITTSBURGH.

XX XX Tracey KJ, Yang H, Warren HS, Fink MP;

XX XX WPI; 2003-120594/11.

XX PT New isolated polypeptide having a vertebrate HMGB A box, useful for

PT inhibiting a condition associated with an activated inflammatory cytokine  
 PT cascade, e.g. endotoxin shock, myocardial infarction, asthma, HIV  
 PT infection, malaria and diabetes.

XX Example 1; Page 37; 82pp; English.

XX The invention relates to high mobility group (HMG) protein comprising DNA  
 CC binding motifs termed HMG A box and HMG B box. HMG A box or a non-  
 CC naturally occurring HMG A box inhibits the release of a pro-inflammatory  
 CC cytokine from a vertebrate cell. The methods and compositions of the  
 CC invention are useful for inhibiting a condition characterised by  
 CC activation of an inflammatory cytokine cascade such as endotoxin shock,  
 CC rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's  
 CC disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,  
 CC sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,  
 CC filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,  
 CC myocardial infarction, meningitis, multiple sclerosis, gout,  
 CC cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host  
 CC disease, diabetes and Hodgkin's disease. The invention is useful in gene  
 CC therapy. The present sequence is human HMGI (also termed as HMGB1)  
 CC protein (carboxy terminus) mutant

XX Sequence 182 AA;

Query Match 100.0%; Score 110; DB 6; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
 |||||  
 DB 89 FKDPNAPKRLPSAFFLFCSE 108

RESULT 14

ADO25936  
 ID ADO25936 standard; protein; 182 AA.

XX ADO25936;

XX 26-AUG-2004 (first entry)

DE Human high mobility group box 1 C-terminal mutant.

XX cytotstatic; gene therapy; vaccine; pharmaceutical composition;  
 KW HMGB B box; high mobility group; immune response; immunostimulation;  
 KW cancer; human; high mobility group box 1; HMGI; cytokine activity;  
 KW mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX WO2004046338-A2.

XX 03-JUN-2004.

XX 19-NOV-2003; 2003WO-US036975.

XX 20-NOV-2002; 2002US-0427848P.

XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.

XX Tracey KJ;

XX WPI; 2004-420625/39.

XX New pharmaceutical composition comprises a polypeptide comprising an HMGB  
 PT B box or its functional variant, useful for stimulating or increasing an  
 PT immune response in an individual or for treating cancer in an individual.

XX Example 1; SEQ ID NO 19; 68pp; English.

XX The invention describes a pharmaceutical composition comprising a  
 CC polypeptide comprising an HMGB (high mobility group box) B box or its

CC functional variant to treat a disease or condition by increasing an  
 CC immune response in an individual administered with the pharmaceutical  
 CC composition. Also described are: an antibody attached to a polypeptide  
 CC comprising an HMGB B box or its functional variant; stimulating or  
 CC increasing an immune response in an individual in need of  
 CC immunostimulation; and treating cancer in an individual. The composition  
 CC is useful for stimulating or increasing an immune response in an  
 CC individual in need of immunostimulation or for treating cancer in an  
 CC individual. This is the amino acid sequence of a human high mobility  
 CC group box 1 (HMGI) C-terminal mutant.

XX Sequence 182 AA;

Query Match 100.0%; Score 110; DB 8; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
 |||||  
 DB 89 FKDPNAPKRLPSAFFLFCSE 108

RESULT 15

ADO71495

ID ADO71495 standard; protein; 182 AA.

XX ADO71495;

XX 26-AUG-2004 (first entry)

DE Human high mobility group box 1 (HMGB1) mutant protein #1.

XX Human; high mobility group box 1; HMGB1; HMGB; HMGB A box; HMGB B box;  
 KW proinflammatory cytokine; weight loss; obesity; inflammation;  
 KW inflammatory cytokine cascade; sepsis; allograft rejection;  
 KW rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;  
 KW chronic obstructive pulmonary disease; psoriasis; pancreatitis;  
 KW peritonitis; burn; myocardial ischaemia; organic ischaemia;  
 KW reperfusion ischaemia; Behcet's disease; graft-versus-host disease;  
 KW Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia;  
 KW mutant; mutein.

XX Homo sapiens.

OS Synthetic.

XX WO2004046345-A2.

XX 03-JUN-2004.

XX 20-NOV-2003; 2003WO-US037507.

XX 20-NOV-2002; 2002US-0427841P.

XX 20-NOV-2002; 2002US-0427846P.

XX (CRIT-) CRITICAL THERAPEUTICS INC.

XX Newman W, O'keefe TL;

XX WPI; 2004-420628/39.

XX New high mobility group box proteins, useful in treating obesity, sepsis,  
 PT rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,  
 PT Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.

XX Example 1; SEQ ID NO 19; 113pp; English.

XX The invention relates to a polypeptide comprising a high mobility group  
 CC box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of  
 CC a proinflammatory cytokine from a cell treated with an HMGB protein. The  
 CC invention also relates to a purified preparation of antibodies that  
 CC specifically bind to the HMGB B box but do not specifically bind to non-B  
 CC box epitopes of HMGB, where the antibodies can inhibit release of a  
 CC proinflammatory cytokine from a cell treated with HMGB, a method for

CC effecting weight loss or treating obesity in a patient, a method of  
CC determining whether a compound inhibits inflammation, a pharmaceutical  
CC composition comprising an HMGB protein or an antibody that binds to the  
CC protein, an agent that inhibits TNF biological activity and a method of  
CC treating a condition in a patient characterised by activation of an  
CC inflammatory cytokine cascade. Effecting weight loss or treating obesity  
CC in a patient comprises administering to the patient an amount of the  
CC polypeptide. The polypeptide, antibodies, composition and methods are  
CC useful in treating obesity and conditions characterised by activation of  
CC an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,  
CC rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,  
CC chronic obstructive pulmonary disease, psoriasis, pancreatitis,  
CC peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion  
CC ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,  
CC ulcerative colitis, multiple sclerosis or cachexia. This sequence  
CC represents a human HMGB1 mutant polypeptide of the invention.  
XX  
SQ Sequence 182 AA;

Query Match 100.0%; Score 110; DB 8; Length 182;  
Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLCSE 20  
Db ||||||||||||||||  
89 FKDPNAPKRLPSAFFLCSE 108

Search completed: April 6, 2006, 10:19:09  
Job time : 25.2763 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 10:19:38 ; Search time 3.81579 Seconds  
(without alignments)  
504.309 Million cell updates/sec

Title: US-10-717-984-23

Perfect score: 110

Sequence: 1 FKDPNAPKRLPSAFLFCSE 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR 80.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	100.0	216	2 S29857	nonhistone chromos
2	103	93.6	170	2 A27853	nonhistone chromos
3	103	93.6	215	1 NSRTH1	nonhistone chromos
4	103	93.6	215	1 S01947	nonhistone chromos
5	103	93.6	215	2 S02826	nonhistone chromos
6	103	93.6	215	2 A28897	nonhistone chromos
7	103	93.6	215	2 I48688	non-histone chromo
8	100	90.9	210	2 S62355	high mobility grou
9	97	88.2	186	2 S30221	nonhistone chromos
10	97	88.2	207	2 JC1129	nonhistone chromos
11	97	88.2	207	2 JC1114	high-mobility grou
12	97	88.2	209	1 NSH0H2	nonhistone chromos
13	97	88.2	210	2 A34719	nonhistone chromos
14	97	88.2	210	2 S54774	high mobility grou
15	95	86.4	49	2 D61510	high mobility grou
16	93	84.5	201	2 I50254	HMG-1 - chicken
17	93	84.5	202	2 S22359	nonhistone chromos
18	91	82.7	215	2 I51067	gene HMG-T2 protei
19	89	80.9	205	2 S26062	nonhistone chromos
20	87	79.1	172	2 A24019	nonhistone chromos
21	87	79.1	204	2 S48708	high-mobility-grou
22	87	79.1	204	2 T01071	high mobility grou
23	84	76.4	186	2 B61611	nonhistone chromos
24	79	71.8	141	2 T09581	probable high mobi
25	77	70.0	157	2 B47150	high mobility grou
26	77	70.0	161	2 S18991	high mobility grou
27	77	70.0	168	2 T03640	high mobility grou
28	76	69.1	393	2 JC6179	dorsal switch prot
29	76	69.1	393	2 S50068	nonhistone chromos

30	75	68.2	126	2 T03375	high mobility grou
31	75	68.2	141	2 T07377	high mobility grou
32	75	68.2	142	2 T02252	high mobility grou
33	75	68.2	152	2 S22309	high mobility grou
34	74	67.3	178	2 T51159	HMG protein [impor
35	73	66.4	149	2 S39556	high mobility grou
36	72	65.5	138	2 F84553	probable HMG prote
37	72	65.5	138	2 T51596	high mobility grou
38	72	65.5	144	2 S40302	high mobility grou
39	72	65.5	154	2 S40122	high mobility grou
40	67	60.9	95	2 T43006	HMG protein 1.1 -
41	67	60.9	312	2 T27004	hypothetical prote
42	66	60.0	200	2 JC4357	HMG1 protein - sea
43	64	58.2	93	2 A35072	nonhistone chromos
44	64	58.2	125	2 T04662	high mobility grou
45	64	58.2	141	2 T51598	high mobility grou

## ALIGNMENTS

### RESULT 1

S29857  
nonhistone chromosomal protein HMG-1 - human  
C:Species: Homo sapiens (man)  
C>Date: 08-Dec-1993 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S29857  
R:Stros, M.; Dixon, G.H.  
Biochim. Biophys. Acta 1172, 231-235, 1993  
A:Title: A retrovirus gene for non-histone chromosomal protein HMG-1.  
A:Reference number: S29857; MUID:93176821; PMID:8439568  
A:Accession: S29857  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-216 <STR>  
A:Cross-references: UNIPARC:UPI00011DFAA; EMBL:L08048; NID:g184250; PIDN:AAA64970.1; PIR  
A>Note: the authors did not translate the codon for residue 1  
C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C:Keywords: chromosomal protein  
F:6-83//Domain: HMG box homology <HMG1>  
F:92-166//Domain: HMG box homology <HMG2>

Query Match 100.0%; Score 110; DB 2; Length 216;  
Best Local Similarity 100.0%; Pred. No. 6.5e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	FKDPNAPKRLPSAFLFCSE	20
DB	89	FKDPNAPKRLPSAFLFCSE	108

### RESULT 2

A27853  
nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)  
C:Species: Crictetus griseus (Chinese hamster)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: A27853  
R:Lee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.  
Nucleic Acids Res. 15, 5051-5068, 1987  
A:Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA ex  
A:Reference number: A27853; MUID:87259986; PMID:3601666  
A:Accession: A27853  
A:Molecule type: mRNA  
A:Residues: 1-170 <LEE>  
A:Cross-references: UNIPROT:P07156; UNIPARC:UPI00001771D5  
C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C:Keywords: chromosomal protein; DNA binding; nucleus  
F:1-38//Domain: HMG box homology (fragment) <HMG1>  
F:47-121//Domain: HMG box homology <HMG2>

Query Match 93.6%; Score 103; DB 2; Length 170;  
Best Local Similarity 95.0%; Pred. No. 6.6e-09;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
 ||||| ||||| ||||| |||||  
 Db 44 FKDPNAPKRPSPAFFLFCSE 63

## RESULT 3

NSRTH1  
 nonhistone chromosomal protein HMG-1 - rat  
 N;Alternate names: 30K heparin-binding protein, brain; amphoterin  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 09-Jul-2004  
 A;Accession: A41175; A27298; A30188; B48771; A48771; C48771  
 R;Meremies, J.; Pihlaskari, R.; Laiinen, J.; Wartiovaara, J.; Rauvala, H.  
 J. Biol. Chem. 266, 16722-16729, 1991  
 A;Title: 30-kDa heparin-binding protein of brain (amphoterin) involved in neurite outgrowth  
 A;Reference number: A41175; MUID:91358468; PMID:1885601  
 A;Accession: A41175  
 A;Molecule type: mRNA  
 A;Residues: 1-215 <MER>  
 A;Cross-references: UNIPROT:P07155; UNIPARC:UPI0000008A6; GB:M64986; NID:G202884; PIDN:  
 A;Note: part of this sequence, including the amino end of the mature protein, was confirmed  
 A;Note: the authors used antibodies to synthetic peptides to demonstrate this protein in  
 h-mobility group proteins  
 R;Paonessa, G.; Frank, R.; Cortese, R.  
 Nucleic Acids Res. 15, 9077, 1987  
 A;Title: Nucleotide sequence of rat liver HMG1 cDNA.  
 A;Reference number: A27298; MUID:88067717; PMID:3684582  
 A;Accession: A27298  
 A;Molecule type: mRNA  
 A;Residues: 1-10,'R',12-82,84-95,97,'AS',100-215 <PAO>  
 A;Cross-references: UNIPARC:UPI0000173984  
 R;Rauvala, H.; Meremies, J.; Pihlaskari, R.; Korkkolainen, M.; Huhtala, M.L.; Panula, P.  
 J. Cell Biol. 107, 2293-2305, 1988  
 A;Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal  
 brain neurons.  
 A;Reference number: A30188; MUID:89066894; PMID:2461949  
 A;Accession: A30188  
 A;Molecule type: protein  
 A;Residues: 2-14,'X',16-21 <RAU>  
 A;Cross-references: UNIPARC:UPI0000173985  
 R;Parkkinen, J.; Raulo, E.; Meremies, J.; Nolo, R.; Kajander, E.O.; Baumann, M.; Rauvala  
 J. Biol. Chem. 268, 19726-19738, 1993  
 A;Title: Amphoterin, the 30-kDa protein in a family of HMG1-type polypeptides. Enhanced  
 A;Reference number: A48771; MUID:93374971; PMID:8366113  
 A;Accession: B48771  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 98-105,'X',107-112 <PA2>  
 A;Cross-references: UNIPARC:UPI0000173986  
 A;Experimental source: postnatal brain  
 A;Note: sequence extracted from NCBI backbone (NCBI:P137788)  
 C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
 C;Keywords: chromosomal protein; DNA binding; nucleus  
 F;2-215/Product: nonhistone chromosomal protein HMG-1 #status experimental <MAT>  
 F;6-83/Domain: HMG box homology <HMG1>  
 F;92-166/Domain: HMG box homology <HMG2>

Query Match 93.6%; Score 103; DB 1; Length 215;  
 Best Local Similarity 95.0%; Pred. No. 8.3e-09;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
 ||||| ||||| ||||| |||||  
 Db 89 FKDPNAPKRPSPAFFLFCSE 108

## RESULT 4

S01947  
 nonhistone chromosomal protein HMG-1 - bovine  
 N;Alternate names: 33k protein; high-mobility-group protein HMG-1  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 30-Sep-1989 #sequence\_revision 22-Apr-1995 #text\_change 09-Jul-2004

C;Accession: S01947; A61611; S10959; I45910  
 R;Kaplan, D.J.; Duncan, C.H.  
 Nucleic Acids Res. 16, 10375, 1988  
 A;Title: Full length cDNA sequence for bovine high mobility group 1 (HMG1) protein.  
 A;Reference number: S01947; MUID:89057489; PMID:3194213  
 A;Accession: S01947  
 A;Molecule type: mRNA  
 A;Residues: 1-215 <KAP>  
 A;Cross-references: UNIPROT:P10103; UNIPARC:UPI000016C31D; EMBL:X12796; NID:G416; PIDN:C  
 R;Walker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.  
 FEBS Lett. 122, 264-270, 1980  
 A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.  
 A;Reference number: A61611; MUID:81138848; PMID:7202717  
 A;Accession: A61611  
 A;Molecule type: protein  
 A;Residues: 2-22,'S',24-40;48-105,'A',107-157,'X',160-193,'D',195 <WAL>  
 A;Cross-references: UNIPARC:UPI0000173987; UNIPARC:UPI0000173988  
 R;Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.  
 FEBS Lett. 267, 139-141, 1990  
 A;Title: High mobility group proteins 1 and 2 bind preferentially to brominated poly(dG-c

A;Reference number: S10726; MUID:90306387; PMID:2365081  
 A;Accession: S10959  
 A;Molecule type: protein  
 A;Residues: 2-22,'X',24-38 <CHR>  
 A;Cross-references: UNIPARC:UPI0000173989  
 R;Pentecost, B.T.; Dixon, G.H.  
 Biosci. Rep. 4, 49-57, 1984

A;Title: Isolation and partial sequence of bovine cDNA clones for the high-mobility-group  
 A;Reference number: I45910; MUID:84128872; PMID:6141822  
 A;Accession: I45910  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 'PGG',119,'V',121-215 <PEN>  
 A;Cross-references: UNIPARC:UPI000016C31E; GB:M26110; NID:G163156; PIDN:AAA30567.1; PID:  
 C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
 C;Keywords: chromosomal protein; DNA binding; duplication; nucleus  
 F;2-215/Product: nonhistone chromosomal protein HMG-1 #status predicted <MAT>  
 F;6-83/Domain: HMG box homology <HMG1>  
 F;92-166/Domain: HMG box homology <HMG2>

Query Match 93.6%; Score 103; DB 1; Length 215;  
 Best Local Similarity 95.0%; Pred. No. 8.3e-09;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
 ||||| ||||| ||||| |||||  
 Db 89 FKDPNAPKRPSPAFFLFCSE 108

## RESULT 5

S02826  
 nonhistone chromosomal protein HMG-1 - human  
 C;Species: Homo sapiens (man)  
 C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-Jul-2004  
 C;Accession: S02826; A33178; G33178  
 R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.  
 Nucleic Acids Res. 17, 1197-1214, 1989  
 A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.

A;Reference number: S02826; MUID:89160247; PMID:2922262  
 A;Accession: S02826  
 A;Molecule type: mRNA  
 A;Residues: 1-215 <WEN>  
 A;Cross-references: UNIPROT:P09429; UNIPARC:UPI00000015ED; EMBL:X12597; NID:G32326; PIDN:  
 R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.  
 Electrophoresis 11, 883-891, 1990  
 A;Title: Development of a database of amino acid sequences for human colon carcinoma prot

A;Reference number: A33178; MUID:91176935; PMID:2079031  
 A;Accession: A33178  
 A;Molecule type: protein  
 A;Residues: 2-13,'XXF' <WAR>  
 A;Cross-references: UNIPARC:UPI00001771D7  
 A;Accession: G33178  
 A;Molecule type: protein

A;Residues: 2-13 'XX', 16-22 <WA2>  
A;Cross-references: UNIPARC:UPI00001771D7  
C;Genetics:  
A;Gene: GDB:HMGI  
A;Cross-references: GDB:133789; OMIM:163905  
A;Map position: 13q12-13q12  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein; DNA binding; nucleus  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 93.6%; Score 103; DB 2; Length 215;  
Best Local Similarity 95.0%; Pred. No. 8.3e-09;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
|||||  
DB 89 FKDPNAPKRPSPAFFLFCSE 108

## RESULT 6

A28897  
nonhistone chromosomal protein HMG-1 - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C;Accession: A28897  
R;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.  
Biochemistry 27, 6159-6163, 1988  
A;Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide sequence  
A;Reference number: A28897; MUID:89050965; PMID:3191113  
A;Accession: A28897  
A;Molecule type: mRNA  
A;Residues: 1-215 <TSU>  
A;Cross-references: UNIPROT:P12682; UNIPARC:UPI000016C6C4; GB:M21683; GB:M21684; NID:g16  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein; DNA binding; nucleus  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 93.6%; Score 103; DB 2; Length 215;  
Best Local Similarity 95.0%; Pred. No. 8.3e-09;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
|||||  
DB 89 FKDPNAPKRPSPAFFLFCSE 108

## RESULT 7

I48688  
non-histone chromosomal high-mobility group 1 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I48688; A55402; I57021  
R;Yotov, W.V.; St-Arnaud, R.  
Nucleic Acids Res. 20, 3516, 1992  
A;Title: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mobility group 1 protein (HMG1).  
A;Reference number: I48687; MUID:92335012; PMID:1630928  
A;Accession: I48688  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-215 <RES>  
A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; EMBL:Z11997; NID:g53381; PIDN  
R;Ferrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.  
J. Biol. Chem. 269, 28803-28808, 1994  
A;Title: The mouse gene coding for high mobility group 1 protein (HMG1).  
A;Reference number: A55402; MUID:95050689; PMID:7961836  
A;Accession: A55402  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-189, E', 191-215 <FER>  
A;Cross-references: UNIPARC:UPI000016CDD6; EMBL:X80457; NID:g620097; PIDN:CAA56631.1; PI  
R;Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.

Mamm. Genome 5, 91-99, 1994  
A;Title: Molecular cloning, expression analysis, and chromosomal localization of mouse HnRNP A1  
A;Reference number: I57021; MUID:94235965; PMID:8180479  
A;Accession: I57021  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-215 <RE2>  
A;Cross-references: UNIPARC:UPI00000008A6; EMBL:U00431; NID:g437101; PIDN:AAA20508.1; PI  
C;Genetics:

C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein  
F;6-83/Domain: HMG box homology <HMG1>  
F;92-166/Domain: HMG box homology <HMG2>

Query Match 93.6%; Score 103; DB 2; Length 215;  
Best Local Similarity 95.0%; Pred. No. 8.3e-09;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
|||||  
DB 89 FKDPNAPKRPSPAFFLFCSE 108

## RESULT 8

S62355  
high mobility group protein 1 - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S62355  
R;Nightingale, K.; Dimitrov, S.; Reeves, R.; Wolffe, A.P.  
EMBO J. 15, 548-561, 1996  
A;Title: Evidence for a shared structural role for HMG1 and linker histones B4 and H1 in nucleosome assembly  
A;Reference number: S62355; MUID:96174815; PMID:8599938  
A;Accession: S62355  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-210 <NIG>  
A;Cross-references: UNIPROT:Q91596; UNIPARC:UPI00000FB3E3; EMBL:U21933; NID:g709958; PIDN  
A;Note: the authors did not translate the codon for residue 1  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
F;6-82/Domain: HMG box homology <HMG1>  
F;91-165/Domain: HMG box homology <HMG2>

Query Match 90.9%; Score 100; DB 2; Length 210;  
Best Local Similarity 90.0%; Pred. No. 2.4e-08;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
|||||  
DB 88 FKDPNAPKRPSPAFFLFCSD 107

## RESULT 9

S30221  
nonhistone chromosomal protein HMG-2B - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C;Accession: S30221  
R;Alexandre, S.; Li, W.W.; Lee, A.S.  
Nucleic Acids Res. 20, 6413, 1992  
A;Title: A human HMG2 cDNA with a novel 3'-untranslated region.  
A;Reference number: S30221; MUID:93117123; PMID:1475204  
A;Accession: S30221  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-186 <ALS>  
A;Cross-references: UNIPROT:P26583; UNIPARC:UPI000016AA6C; EMBL:Z17240; NID:g322334; PIDN  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992  
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
C;Keywords: chromosomal protein  
F;1-60/Domain: HMG box homology (fragment) <HMG>  
F;69-143/Domain: HMG box homology <HMG1>



EMBO J. 14, 1198-1208, 1995  
 A;Title: High mobility group protein 2 functionally interacts with the POU domains of o  
 A;Reference number: S54774; MUID:95237201; PMID:7720710  
 A;Accession: S54774  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-210 <ZWI>  
 A;Cross-references: UNIPROT:P30681; UNIPARC:UPI000016432C; EMBL:Z46757; NID:g609168; PID  
 C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology  
 F;6-83/Domain: HMG box homology <HMG1>  
 F;92-166/Domain: HMG box homology <HMG2>

Query Match 88.2%; Score 97; DB 2; Length 210;  
 Best Local Similarity 94.7%; Pred. No. 7.2e-08;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDPNAPKRLPSAFFLCSE 20  
 ||||| ||||| ||||| |||||  
 Db 90 KDPNAPKRPSPAFFLCSE 108

RESULT 15  
 D61510  
 high mobility group protein 1 - African clawed frog (fragment)  
 C;Species: Xenopus laevis (African clawed frog)  
 C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
 C;Accession: D61510  
 R;Grossberger, D.; Flajnik, M.; Marcuz, A.  
 Comp. Biochem. Physiol. B 98, 127-133, 1991  
 A;Title: Ribosomal and chromosomal protein cDNA clones of Xenopus laevis thymus isolated  
 A;Reference number: A61510; MUID:91284580; PMID:2060276  
 A;Accession: D61510  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-49 <GRO>  
 A;Cross-references: UNIPROT:Q7LZL5; UNIPARC:UPI00001771D3  
 C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology

Query Match 86.4%; Score 95; DB 2; Length 49;  
 Best Local Similarity 89.5%; Pred. No. 3.5e-08;  
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDPNAPKRLPSAFFLCSE 20  
 ||||| ||||| ||||| |||||  
 Db 7 KDPNAPKRPSPAFFLCSE 25

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 Job time : 3.81579 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 6, 2006, 10:13:48 ; Search time 23.6184 Seconds  
(without alignments)  
597.439 Million cell updates/sec

Title: US-10-717-984-23

Perfect score: 110

Sequence: 1 FKDPNAPKRLPSAFFLFCSE 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	100.0	215	2	Q8BQ02_MOUSE
2	104	94.5	208	2	Q80Y21_MOUSE
3	104	94.5	216	2	Q90228_AMENEM
4	103	93.6	132	2	Q5T7C1_HUMAN
5	103	93.6	157	2	Q5T7C2_HUMAN
6	103	93.6	158	2	Q5T7C4_HUMAN
7	103	93.6	162	2	Q5T7C6_HUMAN
8	103	93.6	176	2	Q59GW1_HUMAN
9	103	93.6	178	2	Q8C7C4_MOUSE
10	103	93.6	180	1	HMGI_CRIGR
11	103	93.6	181	2	Q8BNM0_MOUSE
12	103	93.6	182	2	Q5T7C5_HUMAN
13	103	93.6	206	2	Q5BKQ1_MOUSE
14	103	93.6	211	2	Q9NQJ4_HUMAN
15	103	93.6	211	2	Q6P4N5_XENTR
16	103	93.6	211	2	Q7S242_XENLA
17	103	93.6	214	1	HMGI_BOVIN
18	103	93.6	214	1	HMGI_CANFA
19	103	93.6	214	1	HMGI_HUMAN
20	103	93.6	214	1	HMGI_MOUSE
21	103	93.6	214	1	HMGI_PIG
22	103	93.6	214	1	HMGI_RAT
23	103	93.6	214	2	Q9PUK9_CHICK
24	103	93.6	215	2	Q14321_HUMAN
25	103	93.6	215	2	Q5T7C3_HUMAN
26	103	93.6	215	2	Q4R844_MACFA
27	103	93.6	215	2	Q88611_SPAEH
28	103	93.6	215	2	Q88612_SPAEH
29	103	93.6	215	2	Q9QWY6_SPAEH
30	103	93.6	215	2	Q9QX40_SPAEH
31	103	93.6	215	2	Q548R9_RAT

32	103	93.6	215	2	Q58EV5_MOUSE
33	103	93.6	215	2	Q9YH06_CHICK
34	101	91.8	205	2	Q6NX86_BRARE
35	101	91.8	205	2	Q7ZVC6_BRARE
36	100	90.9	199	2	Q4RRH9_TETNG
37	100	90.9	210	2	Q91596_XENLA
38	100	90.9	210	2	Q6GNQ5_XENLA
39	100	90.9	211	1	HMGLX_HUMAN
40	97	88.2	190	2	Q9CT19_MOUSE
41	97	88.2	195	2	Q96J53_HUMAN
42	97	88.2	200	2	Q6Y235_PAGMA
43	97	88.2	201	1	HMGI_CHICK
44	97	88.2	206	1	HMGI_CHICK
45	97	88.2	208	1	HMGI_HUMAN

## ALIGNMENTS

RESULT 1  
Q8BQ02\_MOUSE PRELIMINARY; PRT; 215 AA.  
AC Q8BQ02;  
DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length  
DE enriched library, clone:DL30095009 product:high mobility group box 1,  
DE full insert sequence.  
GN Names:Hmgb1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayaishizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleishmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pasale G., Quackenbush J.,  
RA Schraml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barh G.,  
RA Blake J., Caffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayaishizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RA The FANTOM Consortium  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";

Q58EV5	m high mobi
Q9YH06	gallus gall
Q6NX86	brachydanio
Q7ZVC6	brachydanio
Q4RRH9	tetracodon n
Q91596	xenopus lae
Q6GNQ5	xenopus lae
Q9UGV6	homo sapien
Q9CT19	mus musculu
Q96J53	homo sapien
Q6Y235	pagrus majo
P40618	gallus gall
P26584	gallus gall
P26583	homo sapien





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DR PIR: A60975; A60975..
DR HSP: P07155; 1CKT.
DR SMR; Q90228; 2-84, 90-167.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS00118; HMG_BOX_2; 2.
SQ SEQUENCE 216 AA; 24703 MW; 85E096F85B4EA5C4 CRC64;

Query Match 94.5%; Score 104; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KDPNAPKRLPSAFFLFCSE 20
Db ||||| ||||| ||||| ||||| |||||
91 KDPNAPKRLPSAFFLFCSE 109

RESULT 4
Q5T7C1 HUMAN
ID Q5T7C1 HUMAN PRELIMINARY; PRT; 132 AA.
AC Q5T7C1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE High-mobility group box 1 (Fragment).
GN Names=HMG1; ORFNames=RP11-550P23.1-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL353648; CA115605.1; -; Genomic_DNA.
DR SMR; Q5T7C1; 2-84.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS00118; HMG_BOX_2; 2.
FT NON TER 132
SQ SEQUENCE 132 AA; 15185 MW; C0FAC527E53F9356 CRC64;

Query Match 93.6%; Score 103; DB 2; Length 132;
Best Local Similarity 95.0%; Pred. No. 1.7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
Db ||||| ||||| ||||| ||||| |||||
89 FKDPNAPKRLPSAFFLFCSE 108

RESULT 5
Q5T7C2 HUMAN
ID Q5T7C2 HUMAN PRELIMINARY; PRT; 157 AA.
AC Q5T7C2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)

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DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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GN Names=HMG1; ORFNames=RP11-550P23.1-009;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL353648; CA115604.1; -; Genomic_DNA.
DR SMR; Q5T7C2; 2-84, 89-157.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS00118; HMG_BOX_2; 2.
FT NON TER 157
SQ SEQUENCE 157 AA; 18164 MW; F38343E7F52FC457 CRC64;

Query Match 93.6%; Score 103; DB 2; Length 157;
Best Local Similarity 95.0%; Pred. No. 2e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
Db ||||| ||||| ||||| ||||| |||||
89 FKDPNAPKRLPSAFFLFCSE 108

RESULT 6
Q5T7C4 HUMAN
ID Q5T7C4 HUMAN PRELIMINARY; PRT; 158 AA.
AC Q5T7C4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE High-mobility group box 1.
GN Names=HMG1; ORFNames=RP11-550P23.1-003;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL353648; CA115603.1; -; Genomic_DNA.
DR SMR; Q5T7C4; 2-84, 89-157.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS00118; HMG_BOX_2; 2.
SQ SEQUENCE 158 AA; 18311 MW; 1A438343E7F52FC4 CRC64;

Query Match 93.6%; Score 103; DB 2; Length 158;
Best Local Similarity 95.0%; Pred. No. 2e-08;

```

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20

||||| ||||| ||||| ||||| |||||

Db 89 FKDPNAPKRLPSAFFLFCSE 108

# RESULT 7

ID Q5T7C6\_HUMAN PRELIMINARY; PRT; 162 AA.

AC Q5T7C6; 2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE High-mobility group box 1 (Fragment).

GN Name=HMG1; ORFNames=RP11-550P23.1-002;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Pelan S.; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

RL ENBL; AL353648; CAl15601.1; -; Genomic\_DNA.

DR SMR; Q5T7C6; 2-84, 89-144.

DR GO; GO:0000785; C:nucleus; IEA.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR001135; Highmobility 12.

DR InterPro; IPR000910; HMG\_12\_box.

DR Pfam; PF00505; HMG\_box; 2.

DR PRINTS; PR00886; HIGHMOBILTY12.

DR SMART; SM00398; HMG; 2.

DR PROSITE; PS00353; HMG\_BOX\_1; 1.

DR PROSITE; PS01118; HMG\_BOX\_2; 2.

FT NON TER 162 162

SQ SEQUENCE 162 AA; 18808 MW; 4866095637D6FA88 CRC64;

Query Match 93.6%; Score 103; DB 2; Length 162;

Best Local Similarity 95.0%; Pred. No. 2.1e-08;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20

||||| ||||| ||||| ||||| |||||

Db 89 FKDPNAPKRLPSAFFLFCSE 108

# RESULT 8

Q5SGW1\_HUMAN

ID Q5SGW1\_HUMAN PRELIMINARY; PRT; 176 AA.

AC Q5SGW1; 2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE High-mobility group box 1 variant (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Myeloblast cell line;

RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,

RA Ohara O., Nagase T., Kikuno F.R.;

RT "None Title";

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

DR ENBL; AB208998; BAD92235.1; -; mRNA.

FT NON TER 1 1

SQ SEQUENCE 176 AA; 20164 MW; C31A7039D92649D9 CRC64;

Query Match 93.6%; Score 103; DB 2; Length 176;

Best Local Similarity 95.0%; Pred. No. 2.2e-08;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20

||||| ||||| ||||| ||||| |||||

Db 91 FKDPNAPKRLPSAFFLFCSE 110

# RESULT 9

Q8C7C4\_MOUSE

ID Q8C7C4\_MOUSE PRELIMINARY; PRT; 178 AA.

AC Q8C7C4; 2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 26, Last annotation update)

DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-

DE length enriched library, clone:C920030E14 product:high mobility group

DE box 1, full insert sequence. (Fragment).

GN Name=Hmgbl;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=99279233; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

```
RL Genome Res. 10:1617-1630(2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao K., Nagao K., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitzunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK050659; BAC34367.1; -, mRNA.
DR HSSP; P07156; INHN.
DR SMR; Q8C7C4; 2-84, 93-171.
DR MGI; MGI:96113; Hmgbl.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0030235; F:nitric oxide synthase regulator activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0006810; P:transport; IDA.
DR InterPro; IPR001135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS00353; HMG_BOX_2; 1.
DR PROSITE; PS01118; HMG_BOX_2; 2.
DR NON TER. 178 178
SQ SEQUENCE 178 AA; 20303 MW; 155FD80D52960A62 CRC64;

Query Match 93.6%; Score 103; DB 2; Length 178;
Best Local Similarity 95.0%; Pred. No. 2.3e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFLFCSE 20
DB 89 FKDPNAPKRPSPSAFLFCSE 108

RESULT 10
HMG1_CRIGR STANDARD; PRT; 180 AA.
AC P07156;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE High mobility group protein 1 (HMG-1) (High mobility group protein B1)
DE (Fragment).
GN Name=HMGBl; Synonyms=HMG-1, HMG1;
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetidae; Cricetinae; Cricetulus.
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RESULT 11
QB8NM0 MOUSE
ID QB8NM0_MOUSE PRELIMINARY; PRT; 181 AA.
AC QB8NM0, 2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:C430013M12 product:high mobility group box 1, full
DE insert sequence. (Fragment).
DE Name:Hmgbi;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayaishizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirai L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayaishizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
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RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayaishizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayaishida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tgami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayaishizaki Y.;
RL Submittted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK082902; BAC38678.1; -, mRNA.
DR HSSP; P07156; INHN.
DR SNR; O8BNM0; 2-84, 93-171.
DR MGI; MGI:96113; Hmgbi.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0006810; P:transport; IDA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00305; HMG_box; 2.
DR PRINTS; PRO0886; HIGHMOBILITY2.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS01118; HMG_BOX_2; 2.
FT NON TER 181
SQ SEQUENCE 181 AA; 20648 MW; B31D82055FD80D52 CRC64;

Query Match 93.6%; Score 103; DB 2; Length 181;
Best Local Similarity 95.0%; Pred. No. 2,3e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFLFCSE 20
Db ||||| ||||| ||||| |||||
89 FKDPNAPKRPSPSAFLFCSE 108

RESULT 12
Q57C5 HUMAN
ID Q57C5_HUMAN PRELIMINARY; PRT; 192 AA.
AC Q57C5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE High-mobility group box 1 (Fragment).
GN Name=HMGb1; ORFNames=RP11-550P23.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL353648; CA115602.1; -, Genomic_DNA.
DR SNR; Q57C5; 2-84, 93-171.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
```

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR000135; Highmobility\_12.  
DR InterPro; IPR000910; HMG\_12\_box.  
DR Pfam; PF00505; HMG\_box; 2.  
DR PRINTS; PR00886; HIGHMOBILITY12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS00353; HMG\_BOX\_1; 1.  
DR PROSITE; PS01118; HMG\_BOX\_2; 2.  
FT NON\_TER 192 192  
SQ SEQUENCE 192 AA; 22050 MW; 6A52DB61DA307CLD CRC64;

Query Match 93.6%; Score 103; DB 2; Length 192;  
Best Local Similarity 95.0%; Pred. No. 2.5e-08;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
Db 89 FKDPNAPKRLPSAFFLFCSE 108  
|||||

RESULT 13  
Q5BKQ1 MOUSE  
ID Q5BKQ1 MOUSE PRELIMINARY; PRT; 206 AA.  
AC Q5BKQ1  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Collins E.A., Grouse L.H., Derge J.G.,  
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zerbahn B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Testis;  
RA Director MGC Project;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC090989; AAH0989.1; -; mRNA.  
DR InterPro; IPR010486; HdeA.  
DR InterPro; IPR000135; Highmobility\_12.  
DR InterPro; IPR000910; HMG\_12\_box.  
DR InterPro; IPR012287; Homeodomain-rel.  
DR InterPro; IPR011993; PH type.  
DR InterPro; IPR011991; Wing\_hlx\_DNA\_bd.  
DR Pfam; PF00505; HMG\_box; 2.  
DR PRINTS; PR00886; HIGHMOBILITY12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS01118; HMG\_BOX\_2; 2.

KW Hypothetical protein.  
SQ SEQUENCE 206 AA; 23569 MW; 3F06A32D1A618B98 CRC64;

Query Match 93.6%; Score 103; DB 2; Length 206;  
Best Local Similarity 95.0%; Pred. No. 2.7e-08;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
Db 89 FKDPNAPKRLPSAFFLFCSE 108  
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ID Q9NQJ4 HUMAN PRELIMINARY; PRT; 211 AA.  
AC Q9NQJ4  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE OTTHUMP00000031372.  
GN Name=HMGILL1; ORFNames=RP4-579F20.2-001;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Howden P.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL160176; CAB92731.1; -; Genomic\_DNA.  
DR HSSP; P07155; IHMF.  
DR SNR; Q9NQJ4; 2-84, 93-171.  
DR Ensembl; ENSG00000124097; Homo sapiens.  
DR HGNC; HGNC:4993; HMGILL1.  
DR GO; GO:000785; C:chromatin; IEA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR000135; Highmobility\_12.  
DR InterPro; IPR000910; HMG\_12\_box.  
DR Pfam; PF00505; HMG\_box; 2.  
DR PRINTS; PR00886; HIGHMOBILITY12.  
DR SMART; SM00398; HMG; 2.  
DR PROSITE; PS01118; HMG\_BOX\_2; 2.  
SQ SEQUENCE 211 AA; 24238 MW; D2623FDE00FA8355 CRC64;

Query Match 93.6%; Score 103; DB 2; Length 211;  
Best Local Similarity 95.0%; Pred. No. 2.7e-08;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
Db 89 FKDPNAPKRLPSAFFLFCSE 108  
|||||

RESULT 15  
Q6P4N5 XENTR  
ID Q6P4N5 XENTR PRELIMINARY; PRT; 211 AA.  
AC Q6P4N5  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein MGC75695.  
GN Name=MGC75695;  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; Silurana.  
OX NCBI\_TaxID=8364;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Embryo;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fanev J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063332; AAH63332.1; -; mRNA.
DR HSSP; P07155; IAAB.
DR SNR; Q6PAN5; 2-84, 89-165.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000135; Highmobility_12.
DR InterPro; IPR000910; HMG_12_box.
DR Pfam; PF00505; HMG_box; 2.
DR PRINTS; PR00886; HIGHMOBILITY12.
DR SMART; SM00398; HMG; 2.
DR PROSITE; PS00353; HMG_BOX_1; 1.
DR PROSITE; PS01118; HMG_BOX_2; 2.
KW Hypothetical protein.
SQ SEQUENCE 211 AA; 24479 MW; C32185AD038D9FA3 CRC64;
Query Match 93.6%; Score 103; DB 2; Length 211;
Best Local Similarity 95.0%; Pred. No. 2.7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 FKDPNAPKRLPSAFFLFCSE 20
Db ||||| ||||| ||||| |||||
89 FKDPNAPKRLPSAFFLFCSE 108

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Search completed: April 6, 2006, 10:25:15  
Job time : 26.6184 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:25:39 ; Search time 5.72368 Seconds  
(without alignments)  
288.890 Million cell updates/sec

**Title:** US-10-717-984-23

Perfect score: 110

Sequence: 1 FKDPNAPKRLPSAFLFCSE 20

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scoring card: 3000m2  
Gapop 10.0 , Gapext 0.5

Searched: 572060 segs. 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

100% processing. Minimum Match 0%  
Maximum Match 100%

## Listing first 45 summaries

Database : Issued Patents AA:\*

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3: /cgn2\_6/ptodata/1/iaa/H\_COMB.per:\*

4: /cgn2\_6/prodata/1/iaa/pCTUS\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	103	93.6	214	2	US-09-538-092-883	Sequence 883, App
2	103	93.6	214	2	US-09-214-881A-1	Sequence 1, Appli
3	103	93.6	214	2	US-09-214-881A-3	Sequence 3, Appli
4	103	93.6	214	2	US-09-214-881A-4	Sequence 4, Appli
5	103	93.6	214	2	US-09-214-881A-5	Sequence 5, Appli
6	100	90.9	213	2	US-09-949-016-10813	Sequence 10813, A
7	97	88.2	206	2	US-09-214-881A-9	Sequence 9, Appli
8	97	88.2	208	2	US-09-538-092-1018	Sequence 1018, Ap
9	97	88.2	208	2	US-09-214-881A-2	Sequence 2, Appli
10	97	88.2	209	2	US-09-214-881A-6	Sequence 6, Appli
11	97	88.2	209	2	US-09-214-881A-8	Sequence 8, Appli
12	97	88.2	320	2	US-09-949-016-10728	Sequence 10728, A
13	97	88.2	879	2	US-09-214-259-38	Sequence 38, Appli
14	96	87.3	59	2	US-09-513-999C-4826	Sequence 4826, Ap
15	96	87.3	110	2	US-09-513-999C-4824	Sequence 4824, Ap
16	96	87.3	110	2	US-09-513-999C-4825	Sequence 4825, Ap
17	93	84.5	122	2	US-09-513-999C-4966	Sequence 4966, Ap
18	93	84.5	200	2	US-09-702-705-324	Sequence 324, App
19	93	84.5	200	2	US-09-702-705-789	Sequence 789, App
20	93	84.5	200	2	US-09-736-457-324	Sequence 324, App
21	93	84.5	200	2	US-09-736-457-789	Sequence 789, App
22	93	84.5	200	2	US-09-614-1248-324	Sequence 324, App
23	93	84.5	200	2	US-09-614-1248-789	Sequence 789, App
24	93	84.5	200	2	US-09-671-325-324	Sequence 324, App
25	93	84.5	200	2	US-09-671-325-789	Sequence 789, App
26	93	84.5	200	2	US-09-589-184-324	Sequence 324, App
27	93	84.5	200	2	US-09-589-184-789	Sequence 789, App

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES  
; FILE REFERENCE: 068383.0104  
; CURRENT APPLICATION NUMBER: US/09/214,881A  
; CURRENT FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-214-881A-1

Query Match 93.6%; Score 103; DB 2; Length 214;  
Best Local Similarity 95.0%; Pred. No. 5.2e-09;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
DB 88 FKDPNAPKRPSPSAFFLFCSE 107

## RESULT 3

US-09-214-881A-3  
; Sequence 3, Application US/09214881A  
; Patent No. 6822078

; GENERAL INFORMATION:  
; APPLICANT: Ozaki, Shoichi

; APPLICANT: Sobajima, Junko

; APPLICANT: Uesugi, Hiroko

; APPLICANT: Okazaki, Takahiro

; APPLICANT: Tanaka, Masao

; APPLICANT: Nakao, Kazuo

; APPLICANT: Yoshida, Michiteru

; APPLICANT: Shirakawa, Hitoshi

; APPLICANT: Osakada, Fumio

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES

; FILE REFERENCE: 068383.0104

; CURRENT APPLICATION NUMBER: US/09/214,881A

; CURRENT FILING DATE: 1999-06-07

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 214

; TYPE: PRT

; ORGANISM: Bos taurus

US-09-214-881A-3

Query Match 93.6%; Score 103; DB 2; Length 214;  
Best Local Similarity 95.0%; Pred. No. 5.2e-09;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
DB 88 FKDPNAPKRPSPSAFFLFCSE 107

## RESULT 4

US-09-214-881A-4  
; Sequence 4, Application US/09214881A  
; Patent No. 6822078

; GENERAL INFORMATION:  
; APPLICANT: Ozaki, Shoichi

; APPLICANT: Sobajima, Junko

; APPLICANT: Uesugi, Hiroko

; APPLICANT: Okazaki, Takahiro

; APPLICANT: Tanaka, Masao

; APPLICANT: Nakao, Kazuo

; APPLICANT: Yoshida, Michiteru

; APPLICANT: Shirakawa, Hitoshi

; APPLICANT: Osakada, Fumio

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES

; FILE REFERENCE: 068383.0104

; CURRENT APPLICATION NUMBER: US/09/214,881A

; CURRENT FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 214  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-09-214-881A-4

Query Match 93.6%; Score 103; DB 2; Length 214;  
Best Local Similarity 95.0%; Pred. No. 5.2e-09;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
DB 88 FKDPNAPKRPSPSAFFLFCSE 107

## RESULT 5

US-09-214-881A-5

; Sequence 5, Application US/09214881A

; Patent No. 6822078

; GENERAL INFORMATION:  
; APPLICANT: Ozaki, Shoichi

; APPLICANT: Sobajima, Junko

; APPLICANT: Uesugi, Hiroko

; APPLICANT: Okazaki, Takahiro

; APPLICANT: Tanaka, Masao

; APPLICANT: Nakao, Kazuo

; APPLICANT: Yoshida, Michiteru

; APPLICANT: Shirakawa, Hitoshi

; APPLICANT: Osakada, Fumio

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES

; FILE REFERENCE: 068383.0104

; CURRENT APPLICATION NUMBER: US/09/214,881A

; CURRENT FILING DATE: 1999-06-07

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 214

; TYPE: PRT

; ORGANISM: Rattus rattus

US-09-214-881A-5

Query Match 93.6%; Score 103; DB 2; Length 214;  
Best Local Similarity 95.0%; Pred. No. 5.2e-09;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20  
DB 88 FKDPNAPKRPSPSAFFLFCSE 107

## RESULT 6

US-09-949-016-10813

; Sequence 10813, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10813



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; LENGTH: 213
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10813

Query Match      90.9%; Score 100; DB 2; Length 213;
Best Local Similarity 94.7%; Pred. No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 KDPNAPKRLPSAFLFCS 19
Db  91 KDPNAPKRTPSAFLFCS 109

RESULT 7
US-09-214-881A-9
; Sequence 9, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-214-881A-9

Query Match      88.2%; Score 97; DB 2; Length 206;
Best Local Similarity 94.7%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2 KDPNAPKRLPSAFLFCS 20
Db  89 KDPNAPKRPSPSAFLFCS 107

RESULT 8
US-09-538-092-1018
; Sequence 1018, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapSeqFormatter Version 0.9
; SEQ ID NO 1018
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)

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; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018

Query Match      88.2%; Score 97; DB 2; Length 208;
Best Local Similarity 94.7%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2 KDPNAPKRLPSAFLFCS 20
Db  89 KDPNAPKRPSPSAFLFCS 107

RESULT 9
US-09-214-881A-2
; Sequence 2, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-2

Query Match      88.2%; Score 97; DB 2; Length 208;
Best Local Similarity 94.7%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2 KDPNAPKRLPSAFLFCS 20
Db  89 KDPNAPKRPSPSAFLFCS 107

RESULT 10
US-09-214-881A-6
; Sequence 6, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-214-881A-6

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Query Match 88.2%; Score 97; DB 2; Length 209;  
Best Local Similarity 94.7%; Pred. No. 4.8e-08;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20  
Db 89 KDPNAPKRPSPSAFFLFCSE 107  
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## RESULT 11

US-09-214-881A-8  
; Sequence 8, Application US/09214881A  
; Patent No. 6822078  
; GENERAL INFORMATION:  
; APPLICANT: Ozaki, Shoichi  
; APPLICANT: Sobajima, Junko  
; APPLICANT: Useugi, Hiroko  
; APPLICANT: Okazaki, Takahiro  
; APPLICANT: Tanaka, Masao  
; APPLICANT: Nakao, Kazuo  
; APPLICANT: Yoshida, Michiteru  
; APPLICANT: Shirakawa, Hitoshi  
; APPLICANT: Osakada, Fumio  
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES  
; FILE REFERENCE: 068383.0104  
; CURRENT APPLICATION NUMBER: US/09/214.881A  
; CURRENT FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 209  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-09-214-881A-8

Query Match 88.2%; Score 97; DB 2; Length 209;  
Best Local Similarity 94.7%; Pred. No. 4.8e-08;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20  
Db 89 KDPNAPKRPSPSAFFLFCSE 107  
|||||

## RESULT 12

US-09-949-016-10728  
; Sequence 10728, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949.016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10728  
; LENGTH: 320  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10728

Query Match 88.2%; Score 97; DB 2; Length 320;  
Best Local Similarity 94.7%; Pred. No. 7.7e-08;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20  
Db 201 KDPNAPKRPSPSAFFLFCSE 219  
|||||

## RESULT 13

US-09-914-259-38  
; Sequence 38, Application US/09914259  
; Patent No. 6495336  
; GENERAL INFORMATION:  
; APPLICANT: Makowski, Lee  
; APPLICANT: Hyman, Paul  
; APPLICANT: Williams, Mark  
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
; FILE REFERENCE: 8471-010-999  
; CURRENT APPLICATION NUMBER: US/09/914.259  
; CURRENT FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 879  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-914-259-38

Query Match 88.2%; Score 97; DB 2; Length 879;  
Best Local Similarity 90.0%; Pred. No. 2.3e-07;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20  
Db 763 FKDPNAPKRPPLAFFLFCSE 782  
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## RESULT 14

US-09-513-999C-4826  
; Sequence 4826, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59 US2 REG  
; CURRENT APPLICATION NUMBER: US/09/513.999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4826  
; LENGTH: 59  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-4826

Query Match 87.3%; Score 96; DB 2; Length 59;  
Best Local Similarity 90.0%; Pred. No. 1.8e-08;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20  
Db 38 FKDPNAPKRPSPSAFFLFCSE 57  
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## RESULT 15

US-09-513-999C-4824  
; Sequence 4824, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.

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; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4824
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 91
; OTHER INFORMATION: Xaa=Asp or Gly
US-09-513-999C-4824

Query Match      87.3%; Score 96; DB 2; Length 110;
Best Local Similarity 90.0%; Pred.No. 3.5e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FKDNAPKRLPSAFFLFCSE 20
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Db      89 FKDNAPKRLPSAFFLFCSE 108

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Job time : 6.72368 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:26:34 ; Search time 19.0132 Seconds  
(without alignments)  
439.516 Million cell updates/sec

Title: US-10-717-984-23

Perfect score: 110

Sequence: 1 FKDPNAPKRLPSAFFLFCSE 20

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	100.0	20	4	US-10-147-447-16
2	110	100.0	20	4	US-10-300-072-23
3	110	100.0	20	4	US-10-456-947-16
4	110	100.0	20	4	US-10-456-947-45
5	110	100.0	20	4	US-10-718-495-23
6	110	100.0	20	4	US-10-717-984-23
7	110	100.0	74	4	US-10-147-447-20
8	110	100.0	74	4	US-10-300-072-20
9	110	100.0	74	4	US-10-300-072-53
10	110	100.0	74	4	US-10-456-949-20
11	110	100.0	74	4	US-10-456-947-8
12	110	100.0	74	4	US-10-456-947-39
13	110	100.0	74	4	US-10-718-495-20
14	110	100.0	74	4	US-10-718-495-53
15	110	100.0	74	4	US-10-717-984-20
16	110	100.0	74	4	US-10-717-984-53
17	110	100.0	74	5	US-10-938-992-3
18	110	100.0	74	5	US-10-938-992-69
19	110	100.0	182	4	US-10-147-447-19
20	110	100.0	182	4	US-10-300-072-19
21	110	100.0	182	4	US-10-456-949-19
22	110	100.0	182	4	US-10-718-495-19
23	110	100.0	182	4	US-10-717-984-19
24	110	100.0	216	4	US-10-147-447-18
25	110	100.0	216	4	US-10-300-072-18
26	110	100.0	216	4	US-10-300-072-24
27	110	100.0	216	4	US-10-456-949-18

Sequence 6, Appli  
Sequence 10, Appl  
Sequence 18, Appl  
Sequence 24, Appl  
Sequence 18, Appl  
Sequence 24, Appl  
Sequence 1, Appli  
Sequence 51, Appl  
Sequence 54, Appl  
Sequence 56, Appl  
Sequence 37, Appl  
Sequence 40, Appl  
Sequence 42, Appl  
Sequence 51, Appl  
Sequence 56, Appl  
Sequence 51, Appl  
Sequence 54, Appl

28 110 100.0 216 4 US-10-456-947-6  
29 110 100.0 216 4 US-10-456-947-10  
30 110 100.0 216 4 US-10-718-495-18  
31 110 100.0 216 4 US-10-718-495-24  
32 110 100.0 216 4 US-10-717-984-18  
33 110 100.0 216 4 US-10-717-984-24  
34 110 100.0 216 5 US-10-938-992-1  
35 103 93.6 74 4 US-10-300-072-51  
36 103 93.6 74 4 US-10-300-072-54  
37 103 93.6 74 4 US-10-300-072-56  
38 103 93.6 74 4 US-10-456-947-37  
39 103 93.6 74 4 US-10-456-947-40  
40 103 93.6 74 4 US-10-456-947-42  
41 103 93.6 74 4 US-10-718-495-51  
42 103 93.6 74 4 US-10-718-495-54  
43 103 93.6 74 4 US-10-717-984-51  
44 103 93.6 74 4 US-10-717-984-51  
45 103 93.6 74 4 US-10-717-984-54

#### ALIGNMENTS

##### RESULT 1

US-10-147-447-16

; Sequence 16, Application US/10147447

; Publication No. US20030060410A1

; GENERAL INFORMATION:

; APPLICANT: Tracey, Kevin J.

; APPLICANT: Yang, Huan

; APPLICANT: Warren Jr., Howland Shaw

; APPLICANT: Fink, Mitchell P.

; TITLE OF INVENTION: Use of HMG Fragments as

; FILE REFERENCE: 3268.1001-001

; CURRENT APPLICATION NUMBER: US/10/147,447

; CURRENT FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: 60/291,034

; PRIOR FILING DATE: 2001-05-15

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-147-447-16

Query Match 100.0%; Score 110; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.4e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20

|||||

Db 1 FKDPNAPKRLPSAFFLFCSE 20

##### RESULT 2

US-10-300-072-23

; Sequence 23, Application US/103000072

; Publication No. US20030144201A1

; GENERAL INFORMATION:

; APPLICANT: Kevin J. Tracey

; APPLICANT: Huan Yang

; APPLICANT: Howland Shaw Warren, Jr.

; APPLICANT: Mitchell P. Fink

; TITLE OF INVENTION: USE OF HMG FRAGMENTS AS ANTI-FLAMMATORY

; FILE REFERENCE: 3268.1001-005

; CURRENT APPLICATION NUMBER: US/10/300,072

; CURRENT FILING DATE: 2002-11-20

; PRIOR APPLICATION NUMBER: US 10/147,447

; PRIOR FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: US 60/291,034

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; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-072-23

Query Match      100.0%; Score 110; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
   |||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20
   |||||

RESULT 3
US-10-456-949-16
; Sequence 16, Application US/10456949
; Publication No. US20040005316A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
; FILE REFERENCE: 3268.1001-006
; CURRENT APPLICATION NUMBER: US/10/456,949
; PRIOR FILING DATE: 2003-06-06
; PRIOR FILING DATE: 2002-05-15
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-456-949-16

Query Match      100.0%; Score 110; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
   |||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20
   |||||

RESULT 4
US-10-456-947-45
; Sequence 45, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456,947
; PRIOR FILING DATE: 2003-06-06
; PRIOR FILING DATE: 2002-05-15
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 20
; TYPE: PRT
US-10-456-947-45

Query Match      100.0%; Score 110; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
   |||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20
   |||||

RESULT 5
US-10-718-495-23
; Sequence 23, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
; FILE REFERENCE: 3258.1009-001
; CURRENT APPLICATION NUMBER: US/10/718,495
; CURRENT FILING DATE: 2003-11-12
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-718-495-23

Query Match      100.0%; Score 110; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
   |||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20
   |||||

RESULT 6
US-10-717-984-23
; Sequence 23, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
; FILE REFERENCE: 3258.1008-001
; CURRENT APPLICATION NUMBER: US/10/717,984
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-717-984-23

Query Match      100.0%; Score 110; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSAFFLFCSE 20
   |||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20
   |||||

RESULT 7
US-10-147-447-20
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; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-456-947-8

Query Match      100.0%; Score 110; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 12
US-10-456-947-39
; Sequence 39, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456,947
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-456-947-39

Query Match      100.0%; Score 110; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 13
US-10-718-495-20
; Sequence 20, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
; FILE REFERENCE: 3258.1009-001
; CURRENT APPLICATION NUMBER: US/10/718,495
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/427,841
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-717-984-20

Query Match      100.0%; Score 110; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 14
US-10-718-495-53
; Sequence 53, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3258.1009-001
; CURRENT APPLICATION NUMBER: US/10/718,495
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/427,841
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-718-495-53

Query Match      100.0%; Score 110; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 15
US-10-717-984-20
; Sequence 20, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
; FILE REFERENCE: 3258.1008-001
; CURRENT APPLICATION NUMBER: US/10/717,984
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,846
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-717-984-20

Query Match      100.0%; Score 110; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
Db 1 FKDPNAPKRLPSAFFLFCSE 20

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Job time : 20.0132 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:28:08 ; Search time 2.5 Seconds  
(without alignments)  
249.536 Million cell updates/sec

Title: US-10-717-984-23

Perfect score: 110

Sequence: 1 FKDPNAPKRLPSAFFLFCSE 20

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Total number of hits satisfying chosen parameters: 184161

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /SID55/ptodata/2/pubpaa/US07 NEW PUB pep.\*  
4: /SID55/ptodata/2/pubpaa/PCT NEW PUB pep.\*  
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7: /SID55/ptodata/2/pubpaa/US11 NEW PUB pep.\*  
8: /SID55/ptodata/2/pubpaa/US60 NEW PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	103	93.6	215	7	US-11-186-422-11
3	103	93.6	215	7	US-11-186-422-12
4	97	88.2	169	6	US-10-821-234-1234
5	97	88.2	879	7	US-11-169-041-192
6	79	71.8	69	7	US-11-186-422-14
7	79	71.8	141	7	US-11-087-099-3073
8	77	70.0	160	7	US-11-087-099-1105
9	75	68.2	106	7	US-11-087-099-9185
10	75	68.2	141	7	US-11-087-099-9185
11	75	68.2	142	7	US-11-087-099-4976
12	75	68.2	152	7	US-11-087-099-313
13	75	68.2	152	7	US-11-172-740-1565
14	75	68.2	152	7	US-11-172-740-1566
15	73	66.4	149	7	US-11-087-099-3510
16	73	66.4	149	7	US-11-172-740-1571
17	72	65.5	137	7	US-11-096-568A-3511
18	72	65.5	146	7	US-11-172-740-1569
19	72	65.5	154	7	US-11-087-099-2474
20	72	65.5	154	7	US-11-172-740-1570
21	72	65.5	164	7	US-11-096-568A-3510
22	71	64.5	124	7	US-11-096-568A-9681
23	71	64.5	140	7	US-11-172-740-1564
24	71	64.5	162	7	US-11-096-568A-9680
25	68	61.8	127	7	US-11-096-568A-15615

26	64	61.8	154	7	US-11-096-568A-15614
27	64	58.2	93	7	US-11-087-099-869
28	64	58.2	93	7	US-11-087-099-9518
29	64	58.2	125	7	US-11-172-740-1563
30	64	58.2	145	7	US-11-172-740-1572
31	63	57.3	99	7	US-11-087-099-2564
32	63	57.3	446	7	US-11-087-099-370
33	61	55.5	99	7	US-11-087-099-10060
34	58	52.7	92	7	US-11-087-099-8838
35	58	52.7	108	7	US-11-087-099-6594
36	56.5	51.4	139	7	US-11-096-568A-13611
37	56	50.9	92	7	US-11-087-099-10535
38	56	50.9	139	7	US-11-096-568A-26884
39	56	50.9	149	7	US-11-087-099-11987
40	56	50.9	187	7	US-11-096-568A-26883
41	56	50.9	487	7	US-11-087-099-11126
42	56	50.9	502	7	US-11-087-099-8879
43	53	48.2	372	7	US-11-087-099-6977
44	51	46.4	310	7	US-11-087-099-4210
45	50	45.5	298	7	US-11-087-099-2173

#### ALIGNMENTS

##### RESULT 1

US-10-821-234-1443  
; Sequence 1443, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1443  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1443

Query Match 93.6% Score 103; DB 6; Length 215;

Best Local Similarity 95.0% Pred. No. 3.2e-09;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qv 1 FKDPNAPKRLPSAFFLFCSE 20

Db 89 FKDPNAPKRLPSAFFLFCSE 108

##### RESULT 2

US-11-186-422-11  
; Sequence 11, Application US/11186422  
; Publication No. US20060057679A1  
; GENERAL INFORMATION:  
; APPLICANT: Critical Therapeutics, Inc.  
; APPLICANT: O'Keefe, Theresa  
; APPLICANT: Luciano, Peter  
; APPLICANT: Qin, Shixin  
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES  
; FILE REFERENCE: 3258.1021-003  
; CURRENT APPLICATION NUMBER: US/11/186,422  
; CURRENT FILING DATE: 2005-07-20  
; PRIOR APPLICATION NUMBER: 60/589,678  
; PRIOR FILING DATE: 2004-07-20  
; NUMBER OF SEQ ID NOS: 34

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; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-11

Query Match      93.6%; Score 103; DB 7; Length 215;
Best Local Similarity 95.0%; Pred. No. 3.2e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSPSAFFLFCSE 20
Db 89 FKDPNAPKRPSPSAFFLFCSE 108

RESULT 3
US-11-186-422-12
; Sequence 12, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; FILE REFERENCE: 3258.1021-003
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-186-422-12

Query Match      93.6%; Score 103; DB 7; Length 215;
Best Local Similarity 95.0%; Pred. No. 3.2e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSPSAFFLFCSE 20
Db 89 FKDPNAPKRPSPSAFFLFCSE 108

RESULT 4
US-10-821-234-1234
; Sequence 1234, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1234
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(169)
; OTHER INFORMATION: Xaa = any amino acid or nothing

US-10-821-234-1234
Query Match      88.2%; Score 97; DB 6; Length 169;
Best Local Similarity 94.7%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 KDPNAPKRLPSPSAFFLFCSE 20
Db 77 KDPNAPKRPSPSAFFLFCSE 95

RESULT 5
US-11-169-041-192
; Sequence 192, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 192
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-192

Query Match      88.2%; Score 97; DB 7; Length 879;
Best Local Similarity 90.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FKDPNAPKRLPSPSAFFLFCSE 20
Db 763 FKDPNAPKRPPLAFLFCSE 782

RESULT 6
US-11-186-422-14
; Sequence 14, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-14

Query Match      71.8%; Score 79; DB 7; Length 69;
Best Local Similarity 93.8%; Pred. No. 7.1e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 NAPKRLPSPSAFFLFCSE 20
Db 1 NAPKRPSPSAFFLFCSE 16
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Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
Db 41 KDPNPKRPPSAFFVFME 59

RESULT 10
US-11-087-099-9185
; Sequence 9185, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9185
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-9185

Query Match 68.2%; Score 75; DB 7; Length 141;
Best Local Similarity 73.7%; Pred. No. 6.3e-05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
Db 31 KDPNPKRPPSAFFVFME 49

RESULT 11
US-11-087-099-4976
; Sequence 4976, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4976
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-087-099-4976

Query Match 68.2%; Score 75; DB 7; Length 142;
Best Local Similarity 73.7%; Pred. No. 6.3e-05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
Db 31 KDPNPKRPPSAFFVFME 49

RESULT 12
US-11-087-099-313
; Sequence 313, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 313
; LENGTH: 152
; TYPE: PRT

Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
Db 37 KDPNPKRPPSAFFVFME 55

RESULT 9
US-11-087-099-7075
; Sequence 7075, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7075
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Narcissus pseudonarcissus
US-11-087-099-7075

Query Match 68.2%; Score 75; DB 7; Length 106;
Best Local Similarity 73.7%; Pred. No. 4.7e-05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
Db 37 KDPNPKRPPSAFFVFME 55

RESULT 8
US-11-087-099-1105
; Sequence 1105, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1105
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Hordeum vulgare subsp. vulgare
US-11-087-099-1105

Query Match 70.0%; Score 77; DB 7; Length 160;
Best Local Similarity 73.7%; Pred. No. 3.4e-05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
Db 37 KDPNPKRPPSAFFVFME 55

RESULT 7
US-11-087-099-3073
; Sequence 3073, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3073
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Canavalia gladiata
US-11-087-099-3073

Query Match 71.8%; Score 79; DB 7; Length 141;
Best Local Similarity 75.9%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
Db 32 KDPNPKRPPSAFFVFME 50
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Query Match 66.4%; Score 73; DB 7; Length 149;  
 Best/Local Similarity 68.4%; Pred. No. 0.00014;  
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KDPNAPKRLPSAFFLFCSE 20  
 ||||| ||||| : :  
 Db 40 KDPNKPRLPSAFFVFMAD 58

Search completed: April 6, 2006, 10:33:30  
 Job time : 3.5 secs

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